
MPERLH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run On: Thu Aug 21 09:14:35 1997; MasPar time 1721.16 Seconds
Tabular output not generated. 1336.190 Million cell updates/sec

Title: >US-08-320-157-6
Description: (1-2094) from US08320157.seq
Perfect Score: 2094
N.A. Sequence: 1 GAGGATCTACAGGGACAG.....CAAAAACGAGATCC 2094
Comp: CTCTAGATGTCCTCGTTC.....GTTTTTTTTCCTTAGG

Scoring table: TABLE default
Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 362067 seqs, 549138275 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new3
1: BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV
9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
17:VIR

Database: genbank99
18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7
25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2
31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3
38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10
45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3
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92:ROD8 93:STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3
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105:VRL10
genbank-new3
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112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2
118:ROD 119:SYN 120:UNA 121:VRL
u-emb150_99
122:part1

Statistics: Mean 11.818; Variance 4.529; scale 2.509

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2094	100.0	2094	77	HSU16811	Human Bak mRNA, compl	0.00e+00
2	1899	90.7	6478	77	HSU16812	Human Bak-2 gene, com	0.00e+00
3	1886	90.1	1949	77	HSU23765	Human Bak protein mRN	0.00e+00
4	1496	71.4	5408	77	HSU16813	Human Bak-3 pseudogen	0.00e+00
5	1274	60.8	1360	73	HSCBEP1	H.sapiens BAK mRNA fo	0.00e+00
6	1254	59.9	123579	5	HS291J10	Human DNA sequence **	0.00e+00
7	189	9.0	444	70	D88396S2	Human DNA for apoptosi	7.63e-161
8	90	4.3	140	70	D88396S1	Human DNA for apoptosi	3.06e-58
9	49	2.3	94459	86	MWTSXDNA	M.musculus 94kb genom	1.33e-19
10	38	1.8	215	57	I28278	Sequence 5 from paten	2.15e-10
11	33	1.6	215	57	I28278	Sequence 5 from paten	1.58e-06
12	27	1.3	1782	54	A28072	Mouse brain GAD sequ	2.81e-02
13	25	1.3	45976	73	HSAC000028	00023; HTGS phase 3,	2.81e-02
14	25	1.2	257	77	HSU19554	Human 18q- syndrome b	5.52e-01
15	25	1.2	2754	79	HUMANONYMO	Human anonymous gene,	5.52e-01
16	23	1.1	105	56	I14734	Sequence 13 from pate	9.07e+00
17	24	1.1	105	56	I14734	Sequence 13 from pate	2.29e+00
18	23	1.1	259	72	HS7666F	H.sapiens Cpg island	9.07e+00
19	23	1.1	284	72	HS7666R	H.sapiens Cpg island	9.07e+00
20	23	1.1	421	76	HSPKBI19	H.sapiens PKB gene (9.07e+00
21	24	1.1	1055	85	MMGASTG3	M.musculus gast gene	2.29e+00
22	23	1.1	1260	94	SYNCTCONS	Bacterial cytochrome	9.07e+00
23	24	1.1	1267	97	MMU38136	Mus musculus gastrin	2.29e+00
24	23	1.1	2060	80	HUMGAL16	Human G-alpha 16 prot	9.07e+00
25	22	1.1	2086	84	S52659	lactoferrin [5', regio	3.41e+01
26	22	1.1	2212	118	S82821S1	GSTA5-glutathione S-t	3.41e+01
27	22	1.1	2212	122	S82821	GSTA5-glutathione S-t	3.41e+01
28	24	1.1	2492	84	S49592	transcription factor	2.29e+00
29	24	1.1	2647	85	MMGSTP1	M.musculus (BALB/c) G	2.29e+00
30	24	1.1	2744	86	MMNYC2	Woodchuck intronless	2.29e+00
31	24	1.1	2857	74	HSE2F1S03	Human transcription f	2.29e+00
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34	22	1.1	5374	86	MMU02313	Mus musculus MAST205	3.41e+01
35	24	1.1	5632	41	DROFSHB	D.melanogaster fish me	2.29e+00
36	24	1.1	5931	39	DDU32174	Dictyostelium discoid	2.29e+00
37	22	1.1	6814	75	HSL219F9B	Human DNA sequence fr	3.41e+01
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41	23	1.1	27371	37	CELRI1F4	Caenorhabditis elegans	9.07e+00
42	24	1.1	35609	73	HSCU90B3	Human DNA sequence fr	2.29e+00
43	23	1.1	42501	78	HSV618H1	Human DNA sequence fr	9.07e+00
44	23	1.1	215285	6	HSU91322	Human chromosome 16p1	9.07e+00
45	23	1.1	215285	116	HSU91322	Human chromosome 16p1	9.07e+00

ALIGNMENTS

RESULT	LOCUS	1	HSU16811	2094 bp	mRNA	PRI	19-AUG-1995
DEFINITION	Human Bak mRNA, complete cds.						
ACCESSION	U16811						
NID	9595923						
KEYWORDS	human.						
SOURCE	Homo sapiens						
ORGANISM	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.						
REFERENCE	1 (bases 1 to 2094)						
AUTHORS	Kiefer,M.C., Brauer,M.J., Powers,V.C., Wu,J.J., Umansky,S.R., Tomei,L.D. and Barr,P.J.						
TITLE	Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak						
JOURNAL	Nature 374 (6524), 736-739 (1995)						
MEDLINE	95231654						
REFERENCE	2 (bases 1 to 2094)						
AUTHORS	Kiefer,M.C.						
TITLE	Direct Submission						
JOURNAL	Submitted (02-NOV-1994) Michael C. Kiefer, Mol. Biol., LXR						

Biotechnology Inc., 1401 Marina Way South, Richmond, CA 94804, USA
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 AUTHORS Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
 Tomei L.D., and Barr P.J.
 TITLE Modulation of apoptosis by the widely distributed Bcl-2 homologue
 Bak
 JOURNAL Nature 374 (6524), 736-739 (1995)
 MEDLINE 95231654
 REFERENCE 2 (bases 1 to 5408)
 AUTHORS Kiefer M.C.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1994) Michael C. Kiefer, Mol. Biol., LXR
 Biotechnology Inc., 1401 Marina Way South, Richmond, CA 94804, USA
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Db 3503 cctcctcctcgtagtttggaaataaacttgcgaatcccatcaaaaaaaagagaga 3561
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RESULT 5

LOCUS HSCEBP1 1360 bp RNA PRI 05-MAY-1995

DEFINITION H.sapiens BAK mRNA for BCL-2 homologue.

ACCESSION X84213

NID 9804984

KEYWORDS Bcl-2 protein; CEBP-1 gene.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrates; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1360)

AUTHORS Farrow,S.N., White,J.H., Martinou,I., Raven,T., Pun,K.T.,

Glinham,C.J., Martinou,J.C. and Brown,R.

Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K

Nature 374 (524), 731-733 (1995)

MEDLINE 95231852

REMARK Erratum:[Nature 1995 Jun 1;375(6530):431]]

REFERENCE 2 (bases 1 to 1360)

AUTHORS Brown,R.

TITLE Direct Submission

JOURNAL Submitted (25-JAN-1995) R. Brown, Glaxo Research & Development,

Greenford Road, Greenford, Middlesex UB6 0HE, UK

FEATURES Location/Qualifiers

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QY 252  GCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCAGCAGCAGAGGAGGTTTCCCGCAGC 311
Db 304  taagtttttaccgcacatcgaggaacagagaggtggaaggggtggctgcccctggcagc 363
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OC Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP 1-123579
RA Beck S.;
RT ;
RL Submitted (06-NOV-1996) to the EMBL/GenBank/DBJ databases.
RL Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA,
RL UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests:
RL clonerequest@sanger.ac.uk
CC IMPORTANT: This sequence is unfinished and does not necessarily
CC represent the correct sequence. Work on the sequence is in progress
CC and
CC the release of this data is based on the understanding that the
CC sequence may change as work continues. The sequence may be
CC contaminated
CC with foreign sequence from E.coli, yeast, vector, phage etc.
CC Order of segments is not known: 800 n's separate segments.
CC Unfinished sequence: dJ291J10 Contig_ID: 01371 Length: 3951 bp
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ACCESSION D88397
NID g1655492
KEYWORDS Bak; apoptosis-regulator.
SEGMENT 2 of 2
SOURCE Homo sapiens DNA, clone: pGEMBak01-02.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS Eguchi,H.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hidetaka Eguchi, Saitama Cancer Center Research Institute,
Department of Biochemistry, 818 Komuro, Ina, Kita-adachi-gun,
Saitama 362, Japan (E-mail:hidetaka@saitema-cc.go.jp,
Tel:048-722-1111(ex.255), Fax:048-722-1739)
REFERENCE 2 (bases 1 to 444)
AUTHORS Eguchi,H. and Hayashi,S.
TITLE Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL
and Bak, as well as susceptibility to therapeutic agents of human
breast cancer cells
JOURNAL Unpublished (1996)
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Db 1775 atc 1777
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QY 160 ATC 162

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NID         gl620534
KEYWORDS    HTG; HTGS_PHASE3.
SOURCE      human.
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            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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1 (bases 1 to 45976)
Wang, Z. and Roe, B.A.
completed clone 6e4 from human chromosome 12, 45976 bp
Unpublished (1996)
2 (bases 1 to 45976)
Meltzer, P.
Unpublished (1996)
3 (bases 1 to 45976)
Roe, B.A.
Direct Submission
Submitted (21-OCT-1996) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
FEATURES
source      Location/Qualifiers
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ORIGIN

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ACCESSION    U19554
NID          g1098521
KEYWORDS

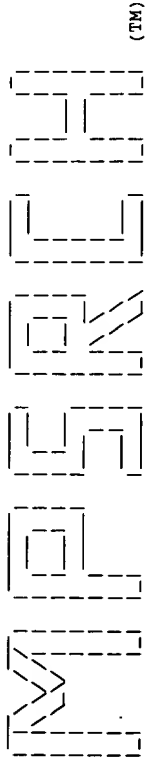
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R*

BASE COUNT 744 a 694 c 723 g 593 t
ORIGIN

Query Match 1.2%; Score 25; DB 79; Length 2754;
Best Local Similarity 68.1%; Pred. No. 5.52e-01;
Matches 47; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Db 229 gatggctgagatcccaagaccctgaagcagcagggtggcgaagtgtggcaatagaaataga 288
Cp 1638 GATGGGTGAGGCCTTCACCTGTAGTGAATGGGTGGGAGCAAGTCTATAAGGAGAGA 1579
Db 289 agaacggag 297
Cp 1578 GGAAGGGAG 1570

Search completed: Thu Aug 21 10:27:37 1997
Job time : 4382 secs.



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Aug 21 10:27:57 1997; MasPar time 218.06 Seconds
Tabular output not generated. 944.863 Million cell updates/sec

Title: >US-08-320-157-6
Description: (1-2094) from US08320157.seq
Perfect Score: 2094
N.A. Sequence: 1 GAGGATCTACAGGGACAAG.....CAAAAGAAAAACGGAGATCC 2094
Comp: CTCCTAGATGTCCTCCCTGTC.....GTTTTTTTTTGCCTCTAGG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 134151 seqs, 49196315 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-genseq27

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 9.693; Variance 5.444; scale 1.780

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2094	100.0	2094	24	T42138	0.00e+00
2	2072	98.9	2072	14	Q95492	0.00e+00
3	1899	90.7	6511	14	Q95493	0.00e+00
4	1886	90.1	1968	19	T17375	0.00e+00
5	1496	71.4	5408	14	Q95494	0.00e+00
6	883	42.2	1286	24	T42139	0.00e+00
7	95	4.5	1047	2	Q10572	0.00e+00
8	78	3.7	1047	2	Q10572	0.00e+00
9	43	2.1	91	9	Q31746	2.35e-34
10	44	2.1	204	1	N81164	1.89e-11
11	45	2.1	204	1	N81164	4.60e-12
12	42	2.0	91	9	Q51746	1.11e-12
13	37	1.8	114	12	Q70465	7.69e-11
14	36	1.7	114	12	Q70465	7.46e-08
15	34	1.6	114	12	Q70466	2.86e-07
16	34	1.6	114	12	Q70465	4.05e-06

17	34	1.6	114	12	Q70469	Generic DNA sequence	4.05e-06
18	34	1.6	114	12	Q70467	Generic DNA sequence	4.05e-06
19	34	1.6	114	12	Q70468	Generic DNA sequence	4.05e-06
c 20	34	1.6	114	12	Q70467	Generic DNA sequence	4.05e-06
c 21	34	1.6	114	12	Q70466	Generic DNA sequence	4.05e-06
c 22	33	1.6	114	12	Q70469	Generic DNA sequence	1.49e-05
c 23	34	1.6	3871	2	N71302	HSV-1 gB and surround	4.05e-06
c 24	31	1.5	114	12	Q70470	Generic DNA sequence	1.95e-04
c 25	32	1.5	114	12	Q70470	Generic DNA sequence	5.44e-05
c 26	29	1.4	114	12	Q70472	Generic DNA sequence	2.38e-03
c 27	30	1.4	114	12	Q70471	Generic DNA sequence	6.87e-04
c 28	29	1.4	114	12	Q70472	Generic DNA sequence	2.38e-03
c 29	28	1.3	114	12	Q70473	Generic DNA sequence	8.11e-03
c 30	27	1.3	114	12	Q70473	Generic DNA sequence	2.71e-02
c 31	27	1.3	1782	5	Q28435	Brain GAD #2.	2.71e-02
c 32	26	1.2	36	2	Q11195	Ballast Constituent c	8.86e-02
c 33	26	1.2	39	7	Q51787	Mixed oligonucleotide	8.86e-02
c 34	25	1.2	74	21	T13613	DC43 TSAR library gen	2.83e-01
c 35	25	1.2	75	21	T13612	DC43 TSAR library gen	2.83e-01
c 36	25	1.2	81	21	T13611	DC43 TSAR library gen	2.83e-01
c 37	25	1.2	82	21	T13610	DC43 TSAR library gen	2.83e-01
c 38	26	1.2	114	12	Q70471	Generic DNA sequence	8.86e-02
c 39	26	1.2	565	6	Q35072	HCV envelope region n	8.86e-02
c 40	25	1.2	565	6	Q35072	HCV envelope region n	8.86e-02
c 41	23	1.1	86	21	T13585	TSAR-9 library genera	2.89e+00
c 42	24	1.1	75	21	T13612	DC43 TSAR library gen	8.85e-01
c 43	24	1.1	82	21	T13610	DC43 TSAR library gen	8.85e-01
c 44	24	1.1	2456	9	Q51137	Retinoblastoma-associ	8.85e-01
c 45	24	1.1	2492	10	Q67603	Retinoblastoma protei	8.85e-01

ALIGNMENTS

RESULT 1
ID T42138 standard; cDNA; 2094 BP.

AC T42138;

DT 22-FEB-1997 (first entry)

DE Bak gene.

KW Human; Bak; apoptosis; latency; virus replication;

KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;

KW drug screening; co-precipitation; ELISA; immunoassay; antibody;

KW protein interactive trapping; virucide; antitumour; diagnostic; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT 5'UTR 1..200

FT /*tag= a

FT CDS 201..836

FT /*tag= b

FT /product= Bak protein

FT 3'UTR 837..2094

FT /*tag= c

PN WO9633416-A1.

PD 24-OCT-1996.

PF 19-APR-1996; U05639.

PR 20-APR-1995; US-426529.

PA (LXRB-) LXR BIOTECHNOLOGY INC.

PI Barr PJ, Kiefer MC;

DR WPI: 96-485886/48.

DR P-PSDB; W03668.

PT Screening for anti-viral agents - by detecting the ability of an

PT agent to disrupt the interaction of a Bak protein and a viral

PT protein

PS Disclosure: Fig 1: 24pp; English.

CC The sequence encodes Bak protein, which is a bcl-1 homologue which

CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

CC protein, and is capable of modulating apoptosis. The Bak gene is

CC located on human chromosome-6 at 6p21-23. The protein may be used

CC in complete or partial form, or as an epitope tag fusion protein,

CC in a new virucide drug screening method, which involves combination

CC of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a

CC test compound, and monitoring for disruption of the interaction,

CC e.g. by co-precipitation, protein interactive trapping or ELISA.

CC Interaction of Bak and viral proteins allows viral replication or

QY 2041 TCTGAGTGTGTGGAATAAATGTCGCAATCCCTCAAAAAAAGCGGAGATCC 2094

RESULT

ID Q95492 standard; cDNA; 2072 BP.
AC Q95492;
DT 21-NOV-1995 (first entry)
DE Human Cdn-1 cDNA.
KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
KW shock; lymphoma; eczema; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 188..903
FT /tag= a
PN WO9515084-A.
PD 08-JUN-1995.
PF 30-NOV-1994; U13930.
PR 30-NOV-1993; U160067.
PR 07-OCT-1994; US-320157.
PA (LXRB-) LAR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC;
DR WPI; 95-215106/28.
DR P-PSDB; R77876.
PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
PT etc.
PS Claim 4; Fig.3A-C; 66pp; English.
CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
CC previously isolated clone as probe. Recombinant Cdn-1 was produced
CC in Sf9 and human colon adenocarcinoma Ht29 cells. Expression of
CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
CC survival in response to anti-Fas-mediated apoptosis.
SQ Sequence 2072 BP; 404 A; 603 C; 598 G; 467 T;

Query Match 98.9%; Score 2072; DB 14; Length 2072;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 2072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ggacaagtaaaagctacatccagatgccgggaatgactgacgagcccatcctggaaactg 60
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QY 14 GCACAAGTAAAGCTACATCCAGATGCCGGGAATGCACATGACGCCCATTCCTGGAAACTG 73
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Db 61 ggtccactagccccctgggagcagcagccagccctcggaacctccatctccacc 120
|||||
QY 74 GGCCTCCACTAGCCCTGGGAGCAGCAGCCGCGCAGCCCTCGGACTCCATCTCCACCC 133
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QY 134 TGTGAGCCACCCGGGTTGGGCCAGGATCCCGCAGGCTGATCCCGCTCTCCACTGAGAC 193
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Db 181 ctgaaaaatggcttcggggcaaggccaggtctctccagcagagagtgcgagagcctac 240
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QY 194 CTGAAAAATGGCTTCGGGCAAGGCCCCAGGTCTCCAGCGAGGATGGGAGAGCCTGC 253
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QY 254 CTTGCCCTCTGCTTCTGAGGAGCAGTAGTACCCAGGACACAGAGAGGTTTTCGACACTA 313
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Db 301 cgtttttaccgccaacagcagaaacagagcgtgaggggtggctgccccgcgagacc 360
|||||
QY 314 CGTATTTTACCCTTACCTAGCAAGAGGAGGCTGAAGGGTGGCTGCCCTGCCGACCC 373
|||||
Db 361 agagatgggtcaccttacctctgcaacctagcagcagcagcagcagcagcagcagcagc 420
|||||
QY 374 AGAGATGGTCACTTACCTCTCAACTTACGACACCATGCGGAGGTGGGACGGCAGCT 433
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Db 421 cgcacatcctgggagcagacatcaaccagcagcagcagcagcagcagcagcagcagcag 480
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QY 434 CGCCATCATCGGGGAGCAGATCAACGACGCTATGACTCAGAGTTCCAGACCATGTGCA 493
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Db 481 gcaactgcagccacggcagagagaatgcctatgagtacttaccacgaattgccaccagcct 540
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QY 494 GCACCTGACGCCACGGCAGAGAATGCCCTATGAGTACTTACCAAGATTCGCCACGAGCT 553
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Db 541 gtttgagagtggcatcaattggggccgctgctgctctctctggcttcgggtaccgctc 600
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QY 554 GTTTGAGAGTGGCATCAATTTGGGGCCGTGTGTGGCTCTTCGCGGCTTCGGGTACCGTCT 613
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Db 601 ggcctacacgtctaccagcatggcctgactggcttctctagccaggtgacccgcttct 660
|||||
QY 614 GGCCTTACACGCTTACCAGCATGGCTGACTGGCTTCTTAGGCCAGGTGACCCGCTTCT 673
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QY 674 GGTGCACTTCACTGCTGCATGCTGCTGCCGGGTGGATTGCACAGAGGGGTGGGTGGGT 733
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Db 721 ggcagccctgaactgggcaatgggtcccatcctgaacgtgctgggtggttctctgggtggt 780
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QY 734 GGCAGCCCTGAACCTTGGGCAATGGTCCCATCTGACAGCTGTGGTGTCTGGGTGGGT 793
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Db 781 tctgtggccagttgtgtgtacgaagattcttcaaatcatgactcccaaggggtgacct 840
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QY 854 TGGGTCCCGGTTTACAGACCCCTGCTGGACTTAAGCGAAGTCTTTCCTTCTCTGTTCCT 913
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Db 901 tgcaggggtcccccctcaagagtacagaagcttttagcaagtgctgactccagcttcctggag 960
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QY 914 TGCAGGGTCCCCCTCAAGAGTACAGAGCTTTAGCAAGTGTGCATCTCCAGTTTCGGAGG 973
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Db 961 cccgtgctggggccagtcagctcagagggcacctcaacattgcatgctgtagtgccc 1020
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QY 974 CCCTGCTGGGGCCAGTCAAGCTGTCAGAGGACCTCAACATTGTCATGCTGTAGTGCCC 1033
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Db 1021 tctctctggggccagggctgtggccgctctctccctcagctctctgggacctcttagccc 1080
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QY 1034 TCTCTCTGGGCCAGGGCTGTGGCCGCTCTCCCTCCCTAGCTCTCTGGGACCTCTTAGCC 1093
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QY 1094 CTGCTCTGTAGCGCTGGGAGACTGATTAACCTTGGGAGGCAAGAGACTGGGAGCCACTT 1153
|||||
Db 1141 ctccccagaaagtgtttaacgggttttagcttttataatccccctgtgagagccctatccc 1200
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QY 1214 CACCATTTACTGTAGGCCAGGACGCTCTGGGTGTGGGATTGGTGGGTCTATGTTCCTCC 1273
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QY 1274 AGATTACGCTATTCTGGAAGATCAGCACCTTAAGAGATGGGACTAGGACCTGAGCCTGG 1333
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QY 1334 TCCCTGGCCGTCCCTTAAGCATGTGTCCAGGACAGGACCTACTAGGAGAGGGGGCCAG 1393
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QY 1394 GTCCCTGCTCAACTACCTTACCCCTGCTCCATTCCTCCCTCGGGCCATACTGCCCTTTCAGT 1453
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QY 1514 TCTGAACCTACGTGTACAGAGGCTTCAAGCCTGCTCCCAAGGTCTCTCAGTTCCTCTCC 1573
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QY 737 AGCCCTGAACCTTGGGCAATGTCCTCCATCCCTGAACGTCTGGTGTCTGGGTGCTCT 796
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 Db 1441 tccct 1500
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 Db 1501 cacccctcctcctggggccttgggttgggttgggttgggttgggttgggttgggttgggt 1560
 QY 1631 CACCC-ATCCCTGGGGGCTTGGGTGAGTGGCCCTGCTAAGGCTCTCTCTTCCCGAGACTA 1699
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 Db 1621 ttctaagtggaagagactatcaaccacttaggaatcccaaggggtgggattcctcctcctc 1680
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 QY 1929 TGCTTCTCTATTGG-CACAGCTAGGGTCTTGGGGTTCAGGGGGAGAGTTCTTCTATT 1987
 Db 1861 cagcccaaatcagggagggagggagcagatggagccatagggccacccctctctctcagtt 1920
 QY 1988 CAGCAAAATCAGGAGGGAGGAGGAGATGGAGCCCATAGGCCATCTCTCTCTGAGT 2047
 Db 1921 gtttggaaataaactgtgcaatccccca 1949
 QY 2048 GTTTGGAAATAAATGTGCAATCCCCCTCA 2076

RESULT 5
 ID Q95494 standard; DNA; 5408 BP.
 AC Q95494;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-3 DNA.
 KW Cdn-3; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
 KW shock; lymphoma; eczema; ss.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT CDS 1665..1931
 FT /*tag= a
 PN WO9515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; UI3930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer WC;
 DR WPI: 95-215106/28.
 DR P-PSDB; R77878.
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure: Fig. 7A-G: 6pp; English.
 CC Southern blot analysis of human genomic DNA and a panel of
 CC human/rodent somatic cell DNAs revealed at least 3 Cdn-related
 CC genes residing on chromosomes 6, 11 and 20. Cdn-3 (R77878)
 CC did not contain the structural features of Cdn-1 (R77876), Cdn-2
 CC (R77877) or other Bcl-2 family members.
 SQ Sequence 5408 BP; 1369 A; 1384 C; 1314 G; 1341 T;

Query Match 71.4%; Score 1496; DB 14; Length 5408;
 Best Local Similarity 89.6%; Pred. No. 0.00e+00;
 Matches 1880; Conservative 0; Mismatches 186; Indels 33; Gaps 23;

Db 1476 ggacaagcaaaaggtacatccagatccagacacccctcagcccttgggaccttcaactcac 1535
 QY 13 GGGCAAGTAAAGGCTACATCCAGATCCGGGAATGACATGACGCCCATCTCTGGAAC 72
 Db 1536 gggctccactcagccctgggagcagcagcctccagcccttgggaccttcaactcac 1595
 QY 73 GGGCTCCACTAGCCCTTGGGAGCAGCAGCCGCCACCCCTCGG-ACCTCCATCTCCAC 131
 Db 1596 cctgctacccacgcgggttggagccagcatccctggaggtgacactgtcctccactgag 1655
 QY 132 CCTGCTAGCACCACCGGTTGGCCAGGATCCCGGAGGCTGATCCCGTCTCTCCACTGAG 191
 Db 1656 acctgaaaaatggcatcgggcaagccagggcctccagggcaggtgcggaaacccct 1715
 QY 192 ACCTGAATAATGGTTCTGGGGCAAGGCCAGGTCTCTCCAGGCAGAGGTGCGGAGACCT 251
 Db 1716 gccctgcccctctctctgtgagggagcaggtagccagagcatggagg-ggttttccgcagc 1774

Qy	252	 GCCCTGCCCCCTTCTGTCTAGGAGCAGGTAGCCCAAGACACAGAGGAGGTTTTCGCAGC	311
Db	1775	tacgttttaccaccatcagcaggaaacaggagctgaaggggcgccgcgcccttcgcccac 	1834
Qy	312	TACGTTTTTACC GCCCATCAGCAGGAACAGAGGCTGAAGGGTGCGTCCCTGCCGAC	371
Db	1835	ccagagatgtcaccttgccccctcaacctagcagcaccaatggyggcaggtygggacggcag 	1894
Qy	372	CCAGAGATGCTACCTTACTCTGCAACCTACGACACCATGGGCGAGTGGGACGGCAG	431
Db	1895	ctgcacataccagg-acacataaacggcactatgacttcggaattccagacaatgct 	1953
Qy	432	CTGCCCATCATCGGGACGACATCAACCGACGCTATGACT-CAGATTGCCAGACCATGTT	490
Db	1954	gcagcacctcagcccacgcgcagagaacccctacagtagtacttccacaagatcgctccag 	2013
Qy	491	GCAGCACCTCGACCCACGCGAGAATGCCATCAGTAGTTCACCAAGATTGCCACGAC	550
Db	2014	cctgtttgaagtggcatcaacccgggcgtgtgtgtgctctctctgtggtctcgactaccg 	2073
Qy	551	CCTGTTTTGAGAGTGGCATCAATTTGGGGCGGTGTGTGGCTCTTCTGGGCTTCGGCTACCG	610
Db	2074	tcgtgtctacatgtctacacacagcgtcttagtgtctctcgtggtctcctggcctggtgacccgtt 	2133
Qy	611	TCGGGCCCTAACGCTTACAGCATGGCCTGACTGGCTTCTTAGGCCAGGTGACCCGCTT	670
Db	2134	cgttgtc---ttcatgtcgaacaaggcatccgcggtggatctcgcagagggcggtcg 	2190
Qy	671	CGTGTGCGACTTCATGCTGCATCTGCTATGCCCGGTGGATTGCACAGAGGGTGCGTG	730
Db	2191	ggtyggacccctggaattgggccaatagtccecatcctgaacgtgtggtgtgggtggtg 	2250
Qy	731	GGTGGCAGCCCTGAACCTTGGCAATGGTCCCATCCTGAACGTGCTGGTGGTCTCTGGGTGT	790
Db	2251	ggttctgtggccagtttgtgtaagaagattcttcaaatcatgactccccaggggtgtc 	2310
Qy	791	GGTTCTGTTGGGCCAGTTGTGTGTAAGAAGATTCTCAAAATCATGACTCCCAAGGGTGCC	850
Db	2311	ctttggggtcccagctgtgaccctgccttggacttaaagccaaagtctttgctctcccact 	2370
Qy	851	CTTTGGG-TCCCGGTTTCAGACCCCTGCTTGAGCTTAACGGAGAGTCTTGGCTTCTCTGTT	909
Db	2371	ccettgcagggtgtcaaccttcaaaagtcagaaagctctagcaaagtgtcacccccgcgtc 	2430
Qy	910	CCCTTGCAGGG-TCCCCCTCAAGAGTACAGAAGCTTTAGCAAAGTGTGCACATCCAGCTTC	968
Db	2431	ggagggccctcgtgtggggccagtcagctcgcgaggacacctcaaatgcacggtgct 	2490
Qy	969	GGAGG--CCCTGGGTGGGGGCCAGTCAGGCTCGCAGAGCACCTCAACATTGCATGTGTGCT	1026
Db	2491	agtygggcccctctctctgtggcccaagggtgtgtgccctcctcccttggctctctgggacctc 	2550
Qy	1027	AGTGCCTCTCTCTGGGCCCCAGGGCTGTGGCCGTCTCTCTCCCTAGCTCTCTGGACCTC	1086
Db	2551	cttagtttgtctgtcagggcgctgcagaggtcgtataacttggggaagcaagagactggga 	2610
Qy	1087	CTTAGCCCTGCTGCTAGGCGCTGGGAGACTGATAAATTGGGGAGGCAAGAGACTGGGA	1146
Db	2611	gcaactcctcccagtaagtgtttaacggttttagctttttataataaccttggggaagc 	2670
Qy	1147	GCCAATTCTCCCCAGAAAGTGTTTAACGGTTTTAGCTTTTTATATACCCCTGTGTGAGAGC	1206
Db	2671	ccattccacattctacccaaggcggatgtctggggtgtggggtgtggtggtcgta 	2730
Qy	1207	CCATTCCACCATCTTACTGTGAGCCAGACGTCGTGGGGTGTGGGGATGTGTGGGTCT-A	1265
Db	2731	acctacgtgccccaggattcagctattctgggaagatcac-agcctaaagactaggaacttg 	2789
Qy	1266	--T- -GTTCCCCAGGATTCAGTATTCTGGAAATCAGCACCCCTAAGAGATGGGACTAG	1320
Db	2790	atcctgggtccttgg--cc-gtccctaagcat-catgtgtccccaggacgagactgactggga 	2846

	QY	1321	GACCTGAGCCTGTGTCCTGGCGCTCCCTAAAGCATGTGTGCCAGGACGAGCACTACTAGGA	1386
	Df	2847	gagggga-ccaaagtctaccaggctcctcccgtgccccattctccc-tccgcacatcc	2904
	QY	1381	GAGGGGGCCAAGTCTTGCTCAACTCTACCCTGTCTCCCATTCTCTCCCTCCGGCCATAC	1440
	Df	2905	tgcctttgcagtttggaactctcacggattcttcgggttgcgggtgtagggcggtgagtaaa	2964
	QY	1441	TGCCTTTGCAAGTTGGACTCTCACGGATTCTCGGGCTTGCGGTGTGGGTGTGGGTGGAGTCG	1500
	Df	2965	caggccagagctctctgaaccttatgtgtcaagaagctctccaagctgctccccaaaggtcct	3024
	QY	1501	CAGACGAGACTGTCTGAACCTCACGTTGTAGAAGCTCCCAAAGCTGCTCCCCAAGGTCCT	1560
	Df	3025	ctcagctctctccctctctctctctctctatatagatacttgtctcccaaaccattcactacagg	3084
	QY	1561	CTCAGTCTCTCCCTTCCCTCTCTCTATAGACACTTGTCTCCCAACCATTCACATCAGG	1620
	Df	3085	tgaagccctcaccccatccctcctgggggaccttgggttgagtgtatgcgctaagccccctcccc	3144
	QY	1621	TGAAGGCTCTFACCCATCCCTTGCGGGCTTGCGGTGAGTAGTGCGCTGTAAGGCTCCTCCTTG	1680
	Df	3145	ccagactacagggcttggtttaggcgcttggtttgatcttatctcagggatagaagagtaggga	3204
	QY	1681	CCCAGACTCAGGGCTT-----AGGACTTGTGTGTATATCAGGGAAAAGGAGTAGGGA	1735
	Df	3205	gttcattctgaaggtttctaagtgaggagaggaactcataaacaccaac-aggaatcccagagg	3263
	QY	1736	GTTTCATCTGGAGGGTCTTAGTGGGAAAGGACTATACAACCACTAGGAATCCACAGAG	1795
	Df	3264	tgggatactccctcataggtctctggcagctgtaatccaggggtggagataggg-aactgt	3322
	QY	1796	TGG-ATCCTCCCTCATGGCTCTGTCACAGTGTATCCAGGGGTGTAGTAGGGGAACGT	1854
	Df	3323	gaatacctgaactgtctccccgaacctcatcgtctcactctcttggtctctctctctca	3382
	QY	1855	GAATACTTGAACTCTGTPTCCCCCAACCTCCATGCTCTCATCTGTCTAGGTCCTCTCAGG	1914
	Df	3383	gtctgggggtgagagtacctctctctcgcagtcacagcctaggggtgttgagggtgaagggg	3442
	QY	1915	GTG-GGGGTGACAGTCCCTTCCTATTGG-CACAGCCTTAGGGTCTTGGGGGTTCAGGGGG	1972
	Df	3443	gagaagtctcttgattcagccaaaatgcaggagggagggcgagaaggagcccaacagggccact	3502
	QY	1973	GAGAAGTCTTGATTTCAGCCAAATGTCAGGGAGGGGAGGCAGATGGAGCCCATAGGCCACC	2032
	Df	3503	ccctatactctagtggtttggaataaactgtgcaatcccatcaaaaaaaaaggagga	3561
	QY	2033	CCCTATCTCTGAGTGTGTGGAATAAATGTGCAATCCCTCAAAAAAAGAACGGAGA	2091
		RESULT	6	
	ID	T42139 standard; cDNA; 1286 BP.		
	AC	T42139;		
	DT	22-FEB-1997 (first entry)		
	DE	Bak-2 gene.		
	KW	Human; Bak-2; apoptosis; latency; virus replication;		
	KW	Eppstein-Barr virus; BHRF1; fusion protein; epitope tag;		
	KW	drug screening; co-precipitation; ELISA; immunoassay; antibody;		
	KW	protein interactive trapping; virucide; antitumour; diagnostic; ds.		
	OS	Homo sapiens.		
	FH	Key	Location/Qualifiers	
	FT	5'UTR	1..543	
	FT	/tag= a	544..1179	
	FT	CDS		
	FT	/tag= b		
	FT	/product= Bak-2 protein		
	FT	3'UTR	1180..1286	
	FT	/tag= c		
	PN	NC_0633416-Al.		
	PD	24-OCT-1996.		
	PF	19-APR-1996; U05639.		
	PR	20-APR-1995; US-426529.		

PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 96-48586/48.
 DR P-PSDB: W03669.
 PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 PS Disclosure; Fig 2; 24pp; English.
 CC The sequence encodes Bak-2 protein, which is a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
 CC protein, and is capable of modulating apoptosis. The Bak-2 gene is
 CC located on human chromosome-20. The protoe protein may be used in
 CC complete or partial form, or as an epitope tag fusion protein, in a
 CC new virucide drug screening method, which involves combination of
 CC Bak-2 protein and a viral protein (e.g. EBV BHRF1), exposure to a
 CC test compound, and monitoring for disruption of the interaction,
 CC e.g. by co-precipitation, protein interactive trapping or ELISA.
 CC Interaction of Bak-2 and viral proteins allows viral replication or
 CC latency in the absence of apoptosis. Compounds which inhibit the
 CC interaction may be used as virucide, antitumour or diagnostic agents.
 SQ Sequence 1286 BP; 298 A; 341 C; 328 G; 319 T;

Query Match 42.2%; Score 883; DB 24; Length 1286;
 Best Local Similarity 98.1%; Pred. No. 0.00e+00;
 Matches 916; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

Db 355 gggacaagtaaaagctacatccagatgctgggaatgcactgacgcccattcctgaaact 414
 QY 13 GGGACAGTAAGGCTACATCCAGATGCCGGGAATGACTGACGCCCATCTCTGGAACCT 72
 Db 415 gggctccactcagccctgggagcagcagccgagccctcgggacccctccatctccac 474
 QY 73 GGGCTCCACTCAGCCCTGSGAGCAGAGCCGCCAGCCCTCGG-ACCTCCATCTCCAC 131
 Db 475 cctgctagccaccocgggttgggcccagatcccgccgggctgattcccgctccactgag 534
 QY 132 CCTGCTGAGCCACCCGGGTTGGGCGCAGGATCCCGGCGAGGCTGATCCCGCTCTCCACTGAG 191
 Db 535 acctgaaataagcttggggcaagcccgaggtctccagcagagagtgaggagagcct 594
 QY 192 ACCTGAANAATGGCTTGGGGCAGGCCCCAGGCTCTCCAGGAGGAGTGGCGGAGCCCT 251
 Db 595 gccctgcccctctgtcttctgaggagcaggtagcccgagcacacagagggaggtttcccgagc 654
 QY 252 GCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCCCAGGACACAGAGGAGGTTTCCCGCAGC 311
 Db 655 tacgtttttaccaccatcagcaggaacagagagctgaagggcggtgcctccctgcgcag 714
 QY 312 TACGTTTTTTTACCGCCCATCAGCAGGAACAGGAGGCTGAAGGGGTGGCTGCCCTGCCGAC 371
 Db 715 ccagagatggtccacttacccttgcacccatagcagcaccatggggcaggtgggacgcag 774
 QY 372 CCAGAGATGCTACCTTACCTTCTCAACCTAGCAGACCATATGGGGCAGGTGGGACGGCAG 431
 Db 775 ctgcccattcattggggcagacatcaaccgagcgtatgactcagaggttccagaccattgtg 834
 QY 432 CTCGCCATCATCGGGAGGACATCAACCGAGCGCTATGACTCAGAGTCCAGACCATGTTG 491
 Db 835 cagcaactgcagccacagcagagagaatgcctatgacttaccacaaagattgcctccagc 894
 QY 492 CAGCACCTGCAGCCGACGGCAGAGAAATGCCCTATGAGTACTTCAACCAAGATTGCCACCAGC 551
 Db 895 ctgtttgagagtgccatcaattggggccgtgtgtgctctcttgggcttccagctaccgt 954
 QY 552 CTGTTTGAGAGTGGCATCAATTTGGGGCGGTGTGTGGCTCTCTCTGCGGTTCGGGTACCGT 611
 Db 955 ctggccctacacatctaccagcgtggcctgactggtcttcttggccaggtgaccgcgttt 1014
 QY 612 CTGGCCCTACAGCTTACCAGCATGGCTGACTGCTCTCTAGGCCAGGTACCCGGTTC 671
 Db 1015 gtggtggaactcatgctgcacatcagtcattgcccgggtgagattgcacagaggggtgcttg 1074
 QY 672 GTGGTGCAGCTTCATGCTGCATCACTGCTATTCGCCGGTGGATTGACACAGAGGGGTGGTGG 731

Db 1075 gtggcagccctgaactgtgggcaatggtcccatcctgaecgtgctgggtgttctgggtgtg 1134
 QY 732 GTGGCAGCCCTGAACCTGGGCAATGGTCCCATCTGAACTGCTGGTGGTTCGGGTGTG 791
 Db 1135 gttctgtgggcccagtttgggtacgaagattctcaaatcatgactcccaagggtgcct 1194
 QY 792 GTTCTGTTGGCCAGTTTGGTACGAAGATTCTCAAAATCATGACTCCCAAGGGTGCCC 851
 Db 1195 ttgggttccagttcagaccctcctgctgacttaagcagagtttggctctctctctctc 1254
 QY 852 TTTGGGTCCCGTTCAGACCCCTGCTGGACTTAAGCGAAGTCTTTGCCCTCTCTGTTC 911
 Db 1255 -ttgcagg-tccccccctcaagatcacagaagctt 1286
 QY 912 CTTGACAGGGTCCCCCTCAAGAGTACAGAAGCTT 945

RESULT 7
 ID Q10572 standard; DNA; 1047 BP.
 AC Q10572;
 DT 03-APR-1991 (first entry)
 DE Human Natriuretic Peptide Receptor B.
 KW NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
 KW hyperaldosteronism; glaucoma; guanyl cyclase.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= signal sequence
 FT Protein 12
 FT /label= mature NPRB
 FT Domain 23..455
 FT /label= extracellular domain
 FT /note= 'binds natriuretic peptides A, B and C'
 FT Domain 456..456
 FT /label= transmembrane domain
 FT Domain 479..1047
 FT /label= cytoplasmic domain
 FT /note= 'GC and protien kinase activity'
 FT Modified -site 24..26
 FT /label= N-glycos_site
 FT Modified -site 35..37
 FT /label= N-glycos_site
 FT Modified -site 161..163
 FT /label= N-glycos_site
 FT Modified -site 195..197
 FT /label= N-glycos_site
 FT Modified -site 244..246
 FT /label= N-glycos_site
 FT Modified -site 277..279
 FT /label= N-glycos_site
 FT Modified -site 349..351
 FT /label= N-glycos_site
 FT Modified -site 600..602
 FT /label= N-glycos_site
 PN W09100292-A.
 PD 10-JAN-1991.
 PF 22-JUN-1990; U03586.
 PR 23-JUN-1989; US-370673.
 PA (GETH) GENENTECH INC.
 PI Chang M, Goeddel D, Lowe D;
 DR WPI: 91-036711/05.
 DR N-PSDB; Q10324.
 PT Natriuretic protein receptor B - for diagnosis and treatment of
 PT kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
 PS Claim 3; Fig 1; 49pp; English.
 CC The sequence was derived from the DNA encoding natriuretic peptide
 CC receptor B. NPRB, having guanyl cyclase (GC) activity and protein
 CC kinase activity. The DNA can be inserted into expression vectors
 CC for the prodn. of the protein, opt. after being mutated to produce
 CC NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-
 CC 114,952). The protein (or variants) can be used in treatment of
 CC natriuretic peptide disorders, and also to isolate peptides using

QY 269 TGAGGAGGAGTAGCCCGAGGACACAGAGAGGTTTTCGCGACTACGTACGTTTTTTACCGCCA 328
 Db 313 nnnrardngvngnsgnmmnagcnydgnnyanvnnntnnggtrdngnrvnkmgr 372
 QY 329 TCAGGAGACAGGAGGCTGAAGGGTGGCTGCCCTGCCACCCAGAG-ATGGTCACCT 387
 Db 373 ygvtnvnmkndndrntdvnwmgdndsgdnnnaahysganknnwtgrtnnnwkgan 432
 QY 388 TACCTCTCAACCTAGCAGCACCATTGGGCGAGGTGGGACGGCAGCTGCCCATCATCGGG 447
 Db 433 nsdnnncandndscdntstnaevangtntnmgvsnnnnrknmknknasnmw 492
 QY 448 ACGACATCAACCGAC-GCTATGACTCAGACTCCAGACCATGTTTCGACACCTGCAGCCC 506
 Db 493 rnrwnnnngnsrnyhkgagartnsnsgsygsmthgkynnnantghnknvvanh 552
 QY 507 ACG-GCAGAGATGCTATGAGTACTTACCAGATTGCCACCGCTGTGTGAGAGTGG 565
 Db 553 vnkkrnntrnvnnnkbnrdvnnnnhtrnngacndnnnnenvntncrgsnnndnnnd- 611
 QY 566 CATCAATTGGGGCGCTGTGGTGGCTTCTGTGGCTTCCGCTACCGTCTGGCCTACACGT 625
 Db 612 anndwmnrynnndnvgmnnhnsnshgnsksncvdsrnnvntdygnasrst 671
 QY 626 CTACGAGCATGGCTGACTGGCTTCTTAGGCCAGGTGACCGCTTCGTGGTGG-ACCTTCA 684
 Db 672 anndnnnnyakntannnnsgnnnttgmnaadvysngnnnnnnnrgnnyngndn 731
 QY 685 TCGTCATCATGCTATGCCCGGTGATGTGCAGAGGGGTGGTGGTGGCAGCCCTGA 744
 Db 732 anknvnkvrntrnynrsndrtnnnnnnnnnrcwandrndnngnknrrnnk 791
 QY 745 ACTTGGCAATGGTCCCATCCTGAACGTGCTGGTGTCTGGTGTCTGTGGTGGCC 804
 Db 792 aggt-snnnnnnrnnnnnnnnknvnrtnsnnnknkanannnnnnhsvannknrgn 850
 QY 805 AGTTTGTGGTACGAAGATCTTCAATCATGACTCCCCAAGGGTGGCCTTGGGTCCCGGT 864
 Db 851 tvnanandsvtnysndvngntansnstnmvntnnndnntcndannndvny-kvntng 909
 QY 865 TC-AGACCCCTGCTGGACTTAAGCGAGTCTTTCCTCTCTGTCTCCTCGCAGGGTCC 923
 Db 910 daymvsgngngrnhrnannmanndavssnrrnhrhndnnrnnrnyhtgnvcagv 969
 QY 924 CCCCTCAAGAGTACAGAAGCTTAGCAAGTGTGCACCTCCAGCTCGGAGGCCCTCGCTGG 983
 Db 970 vgnkmrnyngdvtnt-asrmnsngnnknkhnvsttkd 1007
 QY 984 GGGCAGTCAGGCTGCAGAGGACCTCAACATTGCATGG 1022

RESULT 9
 ID Q51746 standard; cDNA; 91 BP.
 AC Q51746;
 DE 31-MAY-1994 (first entry)
 DT Oligonucleotide probe MK14-A
 KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
 OS Synthetic.
 PN EP-571911-A.
 PD 01-DEC-1993.
 PR 24-MAY-1993; 108325.
 PA (BECT) BECTON DICKINSON CO.
 PI Shank DD, Spears PA;
 DR WPI; 93-37844/48.
 FT New oligo:nucleotide probes specific for Mycobacteria - used for
 PT detection and amplification of Mycobacteria nucleic acid in
 PS samples
 CC Claim 3; Page 14; 23pp; English.
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
 CC cross reacted to a few non-mycobacterial spp. The probe may

CC be useful as an initial screen for mycobacterial infection.
 CC See also Q51735-45 and Q51747-59.
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
 Query Match 2.1%; Score 43; DB 9; Length 91;
 Best Local Similarity 10.2%; Pred. NO. 1.89e-11;
 Matches 6; Conservative 45; Mismatches 8; Indels 0; Gaps 0;
 Db 3 ctccgcgssvhsyvvvvhvshhshhvhvsvvvvhvvhvvhvvhvvhvvhvvhvvc 61
 QY 120 CTCATCTCCACCTGCTGAGCCACCGGGTGGGAGGATCCCGAGGCTGATCCC 178

RESULT 10
 ID N81164 standard; DNA; 204 BP.
 AC N81164;
 DE 08-NOV-1990 (first entry)
 DT Base substituted E.coli beta-galactosidase alpha-fragment.
 KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
 OS Escherichia coli.
 FT Key Location/Qualifiers
 FT misc_feature 19..69
 FT /tag= a
 FT /function-multiple cloning site
 FT primer_bind 187..204
 FT /tag= b
 PN EP-285123-A.
 PD 05-MAY-1988. 105163.
 PR 30-MAR-1988; 105163.
 PR 03-APR-1987; US-034819.
 PA (SUSO) SUOMEN SOKERI OY.
 PI Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
 DR WPI: 88-279927/40.
 PT Introducing random point mutations into nucleic acids -
 PT by prepn of single stranded template, annealing a primer, elongation,
 PT misincorporation, completion of molecules and screening.
 PS Disclosure; p; English.
 CC Random point mutations were introduced into the alpha fragment of
 CC E.coli beta-galactosidase. The wild type sequence was hybridised to a
 CC single stranded template and an oligonucleotide was hybridised to
 CC it to generate a popn of DNA molecules which terminate at all
 CC possible nucleotide positions within a specified region. The
 CC variable 3' ends generated in this way are used as primers for
 CC reverse transcriptase. Nucleotides are misincorporated by the
 CC transcriptase and the molecules are completed to forms that can be
 CC amplified and then expressed in a suitable host-vector system.
 CC The sequence covers all 176 diff base substitutions, most of which
 CC occurred singularly in any given mutant.
 CC See also P80575.
 SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match 2.1%; Score 44; DB 1; Length 204;
 Best Local Similarity 11.2%; Pred. NO. 4.60e-12;
 Matches 13; Conservative 60; Mismatches 43; Indels 0; Gaps 0;
 Db 77 cdchvgcgymrttthyrmrnbvdydnrsdaawycvyrrskdyccynachdhdy 136
 QY 1520 CTCAGGTGTCAAGAGCTCCCAAGGCTGCTCCCAAGGCTCTCAGTCTCTCCCTTCT 1579
 Db 137 vybbvynvnhnnncnccbnhvnbnhvnbnhvnbnhvnbnhvnbnhvnbnhvnbnh 192
 QY 1580 CTCCTCTATAGACACTGTCTCCCAACCCATTCACAGGTGAAGGCTCTCACCC 1635

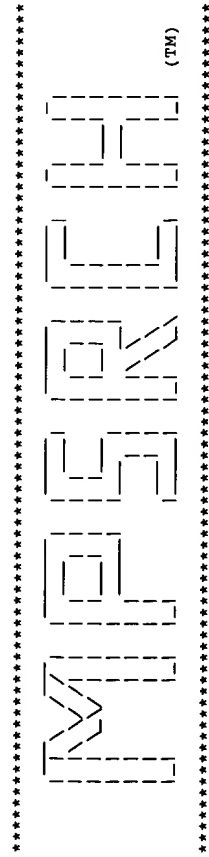
RESULT 11
 ID N81164 standard; DNA; 204 BP.
 AC N81164;
 DE 08-NOV-1990 (first entry)
 DT Base substituted E.coli beta-galactosidase alpha-fragment.
 KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
 OS Escherichia coli.
 FT Key Location/Qualifiers
 FT misc_feature 19..69


```

CP      1778   GGTGTTAGTAGCTTCCACTTCAGAACCTCAGATGAACCTCCCFACTC 17729  

        :|||  

RESULT    13  
ID     Q70465 standard; DNA; 114 BP.  
AC     Q70465;  
DE     05-APR-1995 (first entry)  
KE     Generic DNA sequence to generate a random TSAR petide library.  
KW     TSAR; totally synthetic affinity reagent; synthetic; binding domain;  
       effector domain; concatenated heterofunctional protein; linker;  
       direct; rapid; detection; screening; treatment; generic; ss.  
OS     Synthetic.  
FH     Key Location/Qualifiers  
FT     misc_feature 55..60  
FT     /tag= a  
FT     /note= "this sequence represents 'Z'; Z can be a  
FT     sequence of 6, 9 or 12 nucleotides (see  
FT     comments)"  
PN     WO9418318-A.  
PD     18-AUG-1994.  
PF     01-FEB-1994; UO0977.  
PR     01-FEB-1993; US-013416.  
PR     30-DEC-1993; US-176500.  
PR     31-JAN-1994; US-189331.  
PA     (UYNC-) UNIV NORTH CAROLINA.  
PI     Fowlkes DM, Kay BK,  
WU     WPI: 94-279739/34  
DR     P-PADB; R65150 and R65151.  
PT     Identifying proteins or peptide(s) which bind a ligand - by  
PT     screening a recombinant vector library expressing fusion proteins  
PS     comprising a binding domain and an effector domain  
PS     Disclosure; Page 35; 255pp; English.  
SC     Q70465 is a generic DNA sequence used to generate random TSAR (Totally  
CC     represented as follows: X(NNB)y6(TGC)(X)xilz(NNB)y14(TGC)(NNB)3y.X  
CC     and y are flanking restriction sites (X is not the same as Y) that are  
CC     other specified further. Other generic sequences are shown in Y that are  
CC     other specific peptides generated by these generic sequences are shown in  
CC     R65151-54. TSARS are concatenated heterofunctional proteins or peptides,  
CC     comprising at least two functional regions - a binding domain with  
CC     affinity for a ligand and a second effector peptide portion that is  
CC     chemically or biologically active.They may further comprise a linker  
CC     peptide between the 2 domains.The oligonucleotides are also designed so  
CC     that the expressed peptide contains 2 or 4 cysteine residues positioned  
CC     in, or flanking, the unpredicted or variant residues. These residues  
CC     confer some degree of conformational rigidity to the peptides. The TSARS  
CC     or compans. comprising a TSAR binding domain can be used in vivo to  
CC     deliver a chemically or biologically active moiety, eg. metal ion,  
CC     radioisotope, peptide, toxin or enzyme, to the specific target or on the  
CC     cell. They can also replace the function of macromolecules, eg.  
CC     monoclonal or polyclonal antibodies and therefore circumvent the need  
CC     for complex methods of hybridoma formation or in vivo antibody  
CC     production. The TSARS are easily characterised and have designed  
CC     activity allowing direct and rapid detection in a screening process.  
SQ     Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;  
  
Query Watch 1.8%; Score 37; DB 12; Length 114;  
Best Local Similarity 5.5%; Pred.No. 7.46e-08;  
Matches 6; Conservative 32; Mismatches 71; Indels 0; Gaps 0;
```

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Aug 21 10:38:50 1997; MasPar time 1069.97 Seconds
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Listing first 45 summaries
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27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
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57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
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93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99
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105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
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145:EST145 146:EST146 147:EST147 148:EST148 149:EST149
150:EST150 151:EST151 152:EST152 153:EST153 154:EST154
155:EST155 156:EST156 157:EST157 158:EST158 159:EST159
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165:EST165 166:EST166 167:EST167 168:EST168 169:EST169
170:EST170 171:EST171 172:EST172 173:EST173 174:EST174

Statistics:

Mean 11.801; Variance 2.224; scale 5.307

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	355	17.0	409	84	H52672	yu36g10.r1 Homo sapie	0.00e+00
2	339	16.2	449	84	H52673	yu36g10.s1 Homo sapie	0.00e+00
3	267	12.8	497	155	AA016399	mg88g02.r1 Soares mou	0.00e+00
4	266	12.7	303	85	H56462	yt87a12.r1 Homo sapie	0.00e+00
5	248	11.8	545	153	W42014	mb16g04.r1 Soares mou	0.00e+00
6	229	10.9	446	138	AA049970	mt39b01.r1 Soares mou	0.00e+00
7	154	7.4	161	151	W23886	zb46a10.r1 Soares fet	7.70e-255
8	72	3.4	292	138	AA049828	mt09a09.r1 Soares mou	3.82e-86
9	72	3.4	361	139	AA050569	mt16b12.r1 Soares mou	3.82e-86
10	62	3.0	232	133	N83998	KK4271F Homo sapiens	4.39e-67
11	46	2.2	270	175	W82028	mf02e01.r1 Soares mou	3.69e-38
12	44	2.1	445	126	W77319	me64c04.r1 Soares mou	9.87e-35
13	39	1.9	320	186	AA139013	mt04a06.r1 Soares mou	2.04e-26
14	33	1.6	408	82	H31839	ES1106322 Rattus sp.	5.04e-17
15	31	1.5	279	82	H31840	ES1106323 Rattus sp.	4.50e-14
16	25	1.2	182	99	N62399	yz73c08.s1 Homo sapie	6.17e-06
17	25	1.2	386	2	T58949	yb81f10.r1 Homo sapie	6.17e-06
18	26	1.2	480	5	T70889	yc49b08.s1 Homo sapie	3.32e-07
19	25	1.2	500	61	H15311	ym28b07.r1 Homo sapie	6.17e-06
20	23	1.1	219	22	R39042	ydb7g10.s1 Homo sapie	1.59e-03
21	23	1.1	309	140	C03863	Human Heart cDNA, c10	1.59e-03
22	24	1.1	337	109	HSC3LC012	H. sapiens partial CD	1.04e-04
23	23	1.1	337	145	R85722	yt67d12.s1 Soares ret	1.59e-03
24	23	1.1	338	105	HSB73E022	H. sapiens partial CD	1.59e-03
25	24	1.1	358	133	N92010	za21a11.r1 Homo sapie	1.04e-04
26	23	1.1	368	194	AA189681	zo52f06.r1 Stratagene	1.59e-03
27	23	1.1	368	40	R22823	yh20h06.s1 Homo sapie	1.59e-03
28	23	1.1	377	19	T54824	yb43f08.r1 Homo sapie	1.59e-03
29	23	1.1	391	115	W17230	zb14a04.r1 Soares fet	1.59e-03
30	23	1.1	405	113	W02475	za47d08.r1 Soares fet	1.59e-03
31	23	1.1	406	136	AA001141	zh83c07.r1 Soares fet	1.59e-03
32	24	1.1	409	175	W84628	z891f06.s1 Soares fet	1.04e-04
33	23	1.1	412	159	AA036957	zk32a09.s1 Soares pre	1.59e-03
34	23	1.1	423	188	AA146773	zo35f12.s1 Stratagene	1.59e-03
35	24	1.1	425	147	AA004647	zh92c08.s1 Soares fet	1.04e-04
36	24	1.1	430	41	R25797	yg54b04.r1 Homo sapie	1.04e-04
37	24	1.1	432	53	R92375	yq6g09.r1 Homo sapie	1.04e-04
38	23	1.1	445	174	W80365	z882a03.s1 Soares fet	1.59e-03
39	24	1.1	446	170	W57984	zdl8h07.s1 Soares fet	1.04e-04
40	23	1.1	456	49	HUM519C08B	Human placenta cDNA 5	1.59e-03
41	23	1.1	465	61	H16794	ym39b06.s1 Homo sapie	1.59e-03
42	24	1.1	468	147	AA004387	zh82d01.r1 Soares fet	1.04e-04
43	24	1.1	480	136	AA001756	zh84b09.s1 Soares fet	1.04e-04
44	24	1.1	487	125	W74617	z877e01.s1 Soares fet	1.04e-04
45	23	1.1	641	183	AA097231	mk10f11.r1 Soares mou	1.59e-03

ALIGNMENTS

RESULT 1 H52672 409 bp mRNA EST 18-SEP-1995
LOCUS yu36g10.r1 Homo sapiens cDNA clone 235938 5'
DEFINITION H52672
ACCESSION H52672
NID 9922513
KEYWORDS EST.
SOURCE clone=235938 primer=M13Rpl1 library=Soares ovary tumor NbHOT

vector-p7T3D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) Rsite1-Not I Rsite2-Eco RI Female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 409)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

High quality sequence stops: 307

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..409

/organism="Homo sapiens"

/clone="235938"

<1..>409

73 a 127 c 101 g 101 t 7 others

BASE COUNT

ORIGIN

Query Match 17.0%; Score 355; DB 84; Length 409;
Best Local Similarity 96.1%; Pred. No. 0.00e+00;
Matches 390; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

Db 1 ctatgttccccaggattcagctattcttggaagatcagcacccctaagagatgggactagga 60

Y 1263 CTATGTTCCCCAGGATTTCAGTATTCTGGAGATCAGCACCCCTAAGAGATGGGACTAGGA 1322

D 61 cctgagcctggtcctggcgctccctaaagcatgtgtccaggagcagcactactaggaga 120

Y 1323 CTTGAGCTGTCTGTCGGCGTCCCTAAGCATGTGTCCAGGAGCAGGACCTACTAGGAGA 1382

D 121 ggggggccaaggtctgtcctaacttaccctgtccctattcctccctccggccatactg 180

Y 1383 GGGGGCCCAAGGTCCTGCTCAACTCTACCCCTGCTCCCATCTCTCCCTCCGCCATCTG 1442

D 181 cctttgagttggacttcagggattctggccttggtggtggtngngagtcga 240

Y 1443 CTTTGGCAGTGGGACTCTCAAGGATCTCGGCTTGGGTGTGGGTGGGGTGGAGTCGCA 1502

D 241 gac-agagctgtctgaaactcagtgctcagaagcctcccaagcctcctcccaaggtccct 299

Y 1503 GACCAGACTCTCTGAACCTCAGCTGTGAGAGCCTCCCAAGCCTGCCTCCCAAGGTCTCT 1562

D 300 cagttctctcct 359

Y 1563 CAGTTCTCTCCT 1621

D 360 naaggtctttcacccccctcctgggnccttnggtgagttgcctg 405

Y 1622 GAAGGCTCT-CACCCATC-CCTGGGGGCTTGGGT-GAGTGGCCGTG 1664

RESULT

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

2 H52673 449 bp mRNA EST 18-SEP-1995
Y036410.s1 Homo sapiens cDNA clone 235938 3'.
H52673
9992514
EST.
KEYWORDS
SOURCE

clone=235938 primer=Promega -21ml3 library=Soares ovary tumor
NHOT vector-p7T3D (Pharmacia) with a modified polylinker
host-DH10B (ampicillin resistant) Rsite1-Not I Rsite2-Eco RI
female. 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGGCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified p7T3 vector (Pharmacia). Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 449)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

High quality sequence stops: 379

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

1..449

/organism="Homo sapiens"

/clone="235938"

<1..>449

106 a 127 c 113 g 95 t 8 others

BASE COUNT

ORIGIN

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Best Local Similarity 94.5%; Pred. No. 0.00e+00;
Matches 413; Conservative 0; Mismatches 13; Indels 11; Gaps 11;

D 11 attncacagtttatttccaaacactcagaganaaggggtggcctatggg-tccatctgc 69

Y 2069 ATTGCACAGTTATTTCCTCAACACTCAGAGATAGGGGGTGGCTATGGGCTCCATCTGC 2010

D 70 ctccctccctgcatttggtggaatcaagaactctcccccctgaccccccaagaccctag 129

Y 2009 CTCCTCCCTCCCTGTCATTGGCTGAATCAAGAACTTCTCCCTCCCTGACCCCAAGACCTAG 1950

D 130 gctgtgcaatagagagcactgtcccccacccctcagagacacacacaggtgagg 189

Y 1949 GCTGTGCCAATAGAGAGGCACTGTCAACCCCTCCCTGAGGAGACCTAGACAGGTGAGG 1890

D 190 agcatggaggtgggggaacagagttcaagtattcacagttccccccatctcacacccggg 249

Y 1889 AGCATGGAGGTGGGGGAACAGAGTTCAAGTATTCACAGTTCCCCCATCTACACCCCTGG 1830

D 250 attacactgtgcagagccatgagggaggtacccacactctctgggattccttagtggttg 309

Y 1829 ATTACTGTGCCAGCCATGAGGAGGATCC-ACCTCTGGGATTCTTAGTGG-TGTTG 1772

Email: estevatson.wustl.edu
 High quality sequence stops: 251
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

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FEATURES
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        /organism="Homo sapiens"
        /clone="231262"
      <1..>303
  mRNA
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    ORIGIN
      Query Match 12.7% Score 266; DB 85; Length 303;
      Best Local Similarity 94.7%; Pred. No. 0.00e+00;
      Matches 288; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Db	1	ggcgaggcaatg	nnnctccagcgaggagtg	cggagagcctgcgcctgtattct	60
QY	210	GGGCAAGGCC	AGGTCTCCAGCAGGAGT	GCGAGAGCTGCCCTGCCCTGCTTCT	269
Db	61	gaggagcaggtag	cccgagcacagaggaggttt	ccgcagctacgtttttaccaccat	120
QY	270	GAGGACAGT	AGCCAGGACACAGAGGAGT	TTCCGCAGCTACGTTTTTACCGCCAT	329
Db	121	cagcaggaecag	agggcgtgaaggcgctgc	tgacnc-gaccacagatggcacctta	179
QY	330	CAGCAGGAAC	AGGAGGCTGAAGGGGTGG	CTGCCCTGCCACCCAGAGATGGTACCTTA	389
Db	180	cctctgcaacct	gacgacacatggggcaggt	ggagcgagctgcccatcatggggac	239
QY	390	CTCTGCAACT	AGCAGCACCATGGGGCAGT	GGGCGGAGCTCGCCATCATCGGGGAC	449
Db	240	gacatcaaccg	acgtatgactcagagttcc	agaccatgttncagcacctgcagtcaccac	299
QY	450	GACATCAACC	GCGTATGACTCAGAGT	TTCACACCATGTGTGCAGCACCTGCAG-CCCAC	508
Db	300	ggca	303		
QY	509	GGCA	512		

RESULT	5	W42014	545 bp	EST	11-SEP-1996
LOCUS					
DEFINITION		mb16004.r1 Soares mouse p11MR1.5		Mus musculus cDNA clone 329622	5/
		similar to SW:BC1X_HUMAN Q07817		APOPTOSIS REGULATOR BCL-X.	;
ACCESSION		W42014			
NID		g1326554			
KEYWORDS		EST.			
SOURCE		house mouse.			
ORGANISM		Mus musculus			
		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;			
		Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
		Mus.			

REFERENCE AUTHORS	TITLE JOURNAL
1. (Bases 1 to 545) Marr, M., Haller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gaisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.	The WashU-HMI Mouse EST Project Unpublished (1996)

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL ; con-
IMAGE Consortium (info@image.linl.gov) for further info.
MGI:211022

Possible reversed clone: similarity on wrong strand
Seq primer: ETPrimer
High quality sequence stop: 411.
Location/Qualifiers
1..545
/organism="Mus musculus"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCATCGAAGTCGGCGCGCGATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fátima Bonaldo. RNA was kindly provided by
Dr. Minoru Ku (Wayne State University)."

mrna	BASE COUNT	ORIGIN	134 a	139 c	165 g	105 t	2 others
/rnu_rsc2-2nrob (ampicillin resistant)	<1..>545						

Query Match	11.8%	Score 248;	DB 153;	Length 545;
Best Local Similarity	77.9%	Pred. No. 0.00e+00;		
Matches 381;	Conservative	0;	Mismatches 103;	Indels 5; Gaps 4;

[illegible]

Db 89 **a**ggaatctgtgtaccacgaattggcccaacagAACcaccaccaaaatcacattacggtc 148
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 826 **A**GAATCTTCGTACCAACAAGTGGCCAAACAGAACCACCCCGAAGACCCAGCACGTTTC 767

Db 149 agatgggactctacgaataattcagggtgcaccacccgctctctgtcgatccat 208
||||| | | | | | | | | | | | | | | | | |
Cc 766 AGGATGGGACCAATTGCCAAGCTTCAGGGTGCACCCAGCCCGCCTGCTGCGATCAC 707

[illegible][illegible][illegible]

Db 389 tctaggcattccggcctggggctgaagcgtgtcttagtagattctgggaactctgtgtcg 448

CP 420 TCAATGCGATTCCTGACCCGCTGGGCTGCACATGAGGCTGGAACTCTGAGTCA 48

Db 449 ta -cgccgggtaatatca -ctccgatgagagcaagctgcgacc -acgttgaccaagatg 505

Cp 466 TAGCGTCGGTTGATGTCGTCCCCCGATGATGGGAGCTGCCCGTCCCACCTGCCCCCATGGTG 407
 Db 506 ctgttgggt 514
 |||| | |||

CP 406 CTGCTAGGT 398

RESULT 6

LOCUS	AA049970	446 bp	mrna	EST	09-SEP-1996
DEFINITION	mj39b01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 478441 5' similar to SW:BCIX_HUMAN Q07817 APOPTOSIS REGU				

ACCESSION	AA049970
NID	g1529641

RESULT	6								
LOCUS		AA049970	446 bp	mRNA	EST			09-SEP-1996	
DEFINITION		m339801.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone 478441 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X _L .							
ACCESSION		AA049970							
NID		g1529641							

[illegible]

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QY 1063 CCTCCCTCAGCTCTCTGAGACCTCCTTTAGCCCTCTCTGCTAGCGCTGCGGAGAGACTGATA 1122
Db 61 acttggggaggcaagactggggagccacttctccacagaaagtgtttaacgggttttagc 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1123 ACTTGGGGAGGCAAGAGACTGGGAGCCACTTCTCCACAGAAAGTGTTAACGGTTTATAGC 1182
Db 121 ttttataataacccttggagaagcccaattcccccattct 161
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1183 TTTTATAATACCTTGTGTAGA-GCCCATTCACCACTTCT 1222
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 8
LOCUS AA049828 292 bp mRNA EST 09-SEP-1996
DEFINITION mJ09a09.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone 475576 5'.
ACCESSION AA049828
NID g1529499
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1. (bases 1 to 292)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
TITLE The WashU-HMI Mouse EST Project
JOURNAL
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:286320
Seq primer: -28M13 rev2 from Amersham.
FEATURES
source
1..292
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTGGGAGCGCGCGGAAATTTTATTTTATTTTATTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
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/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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ORIGIN
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Best Local Similarity 79.7%; Pred. No. 3.82e-86;
Matches 137; Conservative 0; Mismatches 29; Indels 6; Gaps 4;

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Db 127 ctcacacaagaccctgaaataatggcatctgtgacaaagaccaggtccccccaggtgggctg 186
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QY 182 CTCACATGACACCTGAAATAATGCTTCGGGGCAAGGCCAGGTCTCTCCAGGAGGAGTG 241
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 187 cgatgaetc--ccc-gtcc-c--cttctgaacagcaggttggccacagacacagaggggt 240
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 242 CGGAGAGCCTGCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCAGGACACAGAGGAGGT 301
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 ctttcgaagctagctttttttacatctccaccagcaggaacagagagacccagggg 292
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 302 TTTCGGCAGCTACGTTTTTTTACCGCCATCAGCAGGAGGAACAGGAGGCTGAAGGG 353
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
LOCUS AA050569 361 bp mRNA EST 09-SEP-1996
DEFINITION mJ16b12.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone 476255 5'.
ACCESSION AA050569
NID g1530241
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1. (bases 1 to 361)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
TITLE The WashU-HMI Mouse EST Project
JOURNAL
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:286999
Seq primer: -28M13 rev2 from Amersham.
FEATURES
source
1..361
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTGGGAGCGCGCGGAAATTTTATTTTATTTTATTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
/clone="476255"
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/lab_host="DH10B"
<1...>361
BASE COUNT 87 a 108 c 103 g 63 t
ORIGIN
Query Match 3.4%; Score 72; DB 139; Length 361;
Best Local Similarity 79.7%; Pred. No. 3.82e-86;

```

[illegible]

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Release 2.1D John F. Collins, BioComputing Research Unit.
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Run on: Thu Aug 21 11:29:58 1997; MasPar time 554.19 Seconds
Tabular output not generated. 1038.366 Million cell updates/sec

Title: >US-08-320-157-6
Description: (1-2094) from US08320157.seq
Perfect Score: 2094
N.A. Sequence: 1 GAGGATCTACAGGGACAAG.....CRAAAAAAAAAACGGAGATCC 2094
Comp: CTCCTAGATGTCCTCGTTC.....GTTTTTTTTTGCCTAGG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 359085 seqs, 137405154 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS-THREE
1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204
7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210
13:EST211 14:EST212 15:EST213 16:EST214 17:EST215
18:EST216 19:EST217 20:EST218 21:EST219 22:EST220
23:EST221 24:EST222 25:EST223 26:EST224 27:EST225
28:EST226 29:EST227 30:EST228 31:EST229 32:EST230
33:EST231 34:EST232 35:EST233 36:STS1 37:STS2 38:STS3
39:STS4 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
46:STS11 47:STS12 48:STS13
EST-STS-FOUR
49:gnEST1 50:gnEST2 51:gnEST3 52:gnEST4 53:gnEST5
54:gnEST6 55:gnEST7 56:gnEST8 57:gnEST9 58:gnEST10
59:gnEST11 60:gnEST12 61:gnEST13 62:gnEST14 63:gnEST15
64:gnEST16 65:gnEST17 66:gnEST18 67:gnEST19 68:gnEST20
69:gnEST21 70:gnEST22 71:gnEST23 72:gnEST24 73:gnEST25
74:gnSTS 75:gnEST1 76:gnEST2 77:gnEST3 78:gnEST4
79:gnEST5 80:gnEST6 81:gnEST7 82:gnEST8 83:gnEST9
84:gnEST10 85:gnEST11 86:gnEST12 87:gnEST13 88:gnEST14
89:gnEST15 90:gnEST16 91:gnEST17 92:gnEST18 93:gnEST19
94:gnEST20 95:gnEST21 96:gnEST22 97:gnEST23 98:gnEST24
99:gnEST25 100:gnEST26 101:gnEST27 102:gnEST28
103:gnEST29 104:gnEST30 105:gnEST31 106:gnSTS 107:ueEST1
108:ueEST2

Database:

Statistics: Mean 11.796; Variance 2.211; scale 5.335

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1248	59.6	1258	38	G06794	human STS WI-7983.	0.00e+00
2	154	7.4	161	88	HS886334	zB46a10.r1 Soares fet	1.68e-256
3	55	2.6	133	91	MM1142620	mt62a08.r1 Soares 2Nb	9.33e-55
4	55	2.6	133	61	AA185611	mt62a08.r1 Soares 2Nb	9.33e-55
5	55	2.6	133	13	AA185611	mt62a08.r1 Soares 2Nb	9.33e-55
6	44	2.1	309	60	AA222196	mw21g06.r1 Soares mou	3.05e-35
7	44	2.1	309	91	MM1141069	mw21g06.r1 Soares mou	3.05e-35
8	42	2.0	498	67	AA242472	mx26g11.r1 Soares mou	7.47e-32
9	42	2.0	498	92	MM1158998	mx26g11.r1 Soares mou	7.47e-32
10	40	1.9	310	7	AA123834	mp93c04.r1 Soares 2Nb	1.60e-28
11	40	1.9	310	98	MM123834	mp93c04.r1 Soares 2Nb	1.60e-28
12	40	1.9	310	58	AA123834	mp93c04.r1 Soares 2Nb	1.60e-28
13	39	1.9	320	56	AA139013	mp04a06.r1 Soares mou	6.98e-27
14	39	1.9	331	108	MM1139075	mv25f11.r1 Barstead m	6.98e-27
15	39	1.9	331	49	AA220617	mw21a06.r1 Soares mou	6.98e-27
16	39	1.9	341	91	MM1141049	mw21a06.r1 Soares mou	6.98e-27
17	39	1.9	341	60	AA222225	z114c11.s1 Soares pre	2.71e-06
18	25	1.2	410	8	AA129872	yyv64f10.r1 Soares fet	7.19e-04
c 19	23	1.1	99	25	N58693	D. melanogaster STS d	9.94e-03
c 20	23	1.1	156	36	DM36D7S	FB17G10 Fetal brain,	9.94e-03
c 21	22	1.1	222	53	T02955	human STS SHGC-16013.	9.94e-03
c 22	22	1.1	250	41	G15328	mo63f04.r1 Stratagene	9.94e-03
c 23	22	1.1	347	55	AA089066	yyv51e02.s1 Soares fet	4.65e-05
c 24	24	1.1	412	25	N59408	mp42f02.r1 Barstead M	9.94e-03
c 25	22	1.1	418	33	AA110168	ze15d02.s1 Soares fet	9.94e-03
c 26	22	1.1	424	89	HSW3043	ze15d02.s1 Soares fet	9.94e-03
c 27	22	1.1	424	1	W92304	ze15d02.s1 Soares fet	9.94e-03
c 28	22	1.1	425	25	N58738	yy74d09.s1 Soares fet	9.94e-03
c 29	24	1.1	442	8	AA126907	z187b04.s1 Stratagene	4.65e-05
c 30	22	1.1	450	25	N57654	yy54d04.s1 Soares fet	9.94e-03
c 31	24	1.1	454	29	AA033526	zf01b10.s1 Soares fet	4.65e-05
c 32	22	1.1	460	21	AA018827	ze57e11.s1 Soares ret	9.94e-03
c 33	23	1.1	465	42	G21837	human STS WI-11990.	7.19e-04
c 34	22	1.1	467	21	AA020955	z664h11.s1 Soares ret	9.94e-03
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c 36	23	1.1	501	73	AA259189	nc34h03.r1 NCI CGAP P	7.19e-04
c 37	22	1.1	534	104	MM1A85558	mt62e08.r1 Soares 2Nb	9.94e-03
c 38	22	1.1	534	61	AA185558	mt62e08.r1 Soares 2Nb	9.94e-03
c 39	22	1.1	534	13	AA185558	mt62e08.r1 Soares 2Nb	9.94e-03
c 40	24	1.1	533	4	AA155608	zk89a06.r1 Soares pre	4.65e-05
c 41	24	1.1	560	4	AA115474	zk89a06.r1 Soares pre	4.65e-05
c 42	22	1.1	600	25	N58258	yyv67g01.s1 Soares fet	9.94e-03
c 43	22	1.1	610	41	G15924	human STS CHLC.UTR.03	9.94e-03
c 44	22	1.1	676	25	N53559	yy43f09.s1 Soares fet	9.94e-03
c 45	22	1.1	1124	38	G07120	human STS WI-9107.	9.94e-03

ALIGNMENTS

RESULT	1	G06794	1258 bp	DNA	STS	19-OCT-1995
LOCUS	human STS WI-7983.					
DEFINITION	G06794					
ACCESSION	g860039					
NID	STS sequence; primer; sequence tagged site.					
KEYWORDS	human STSs derived from sequences in dbEST and the Unigene collection.					
SOURCE	Homo sapiens					
ORGANISM	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 1258)					
AUTHORS	Hudson,T.					
TITLE	Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs					
JOURNAL	Unpublished (1995)					
COMMENT	Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research					

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: CTGATAACTTGGGGAGGCAA

Primer B: GAGAGTCCAACCTGCAAGGC

STS size: 345

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 nM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from U16811 -- Unigene.

FEATURES

source

STS

primer_bind

primer_bind

BASE COUNT

ORIGIN

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281..300
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complement(606..625)
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236 a 356 c 355 g 301 t 10 others
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Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 1248; Conservativeness 0; Mismatches 10; Indels 0; Gaps 0;
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QY 897 TGCCTTCTCTGTTCCCTTGACGGGTCCCCCTCAAGAGTACAGAAGCTTTAGCAAGTGTG 956
Db 121 cactccagcttcggagccctgcgtggggccagtcaggctcagagagccctcaaat 180
QY 957 CACFCCAGCTTCGAGAGCCCTGCTGGGGCCAGTCAGGCTGCAGAGGCACCTCAACATT 1016
Db 181 gcatggtgtagtgcct 240
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QY 1077 CTGGGACCTCTTACGCTGCTGCTAGGCGCTGGGAGAGTACTTGGGGAGGCAA 1136
Db 301 gagactgggagccact 360
QY 1137 GAGACTGGGAGCCACTCTCTCCCCAGAAGTGTAAAGCGTTTATAGCTTTTATAATACC 1196
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Db 421 gtgggtctatgttccccaggattcagctattcttggaagatcagacccttaagagatg 480
QY 1257 GTGGGTCTATGTTCCCCAGGATTTCAGCTATTCTGGAAGATCAGACCCCTAAGAGATGGA 1316
Db 481 ctaggacctgagcctgttctctggtccgtccctcctcctcctcctcctcctcctcctcct 540
QY 1317 CTAGGACCTGAGCCTGGTCTGCGCGTCCCTAAGCATGTGTCCAGAGCAGACCTACT 1376
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QY 1377 AGGAGAGGGGGGCCAAGGTCTCTCACTCTACCCCTGCTCCCATCTCTCCCTCCGGCC 1436
Db 601 atactgcctttgcagttgactctcaggtgattctgggtctgggtggtggtggtggtggtg 660
QY 1437 ATACTGCCTTTGCAGTTGGACTCTCAGGGATTCTGGGCTTGGGCTTGGGCTGGGTTGA 1496
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QY 1737 TTCATCTGGAGGTTCTTAGTGGGAGAGAGACTATCAACACACTAGGAATCCAGAGGT 1796
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Db 1081 ggggggtgacagtgccttct 1140
QY 1917 GGGGGGTGACGTGCTTCTCTATTTGGCAGAGCTTAGGCTTTGGGGGTGAGGGGGAGA 1976
Db 1141 agttcttgattcagcccaaatgcaggaggaggagagagagagagagagagagagagagagag 1200
QY 1977 AGTTCTTGAATCAGCAAAATGAGGGAGGGAGGAGAGTGGAGCCCATAGAGCCACCCCT 2036
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RESULT

2

ID HS886334 standard; RNA; EST; 161 BP.

AC WJ3886;

NI g1300701

DT 09-MAY-1996 (Rel. 47, Created)

DT 07-MAR-1997 (Rel. 51, Last updated, Version 2)

DE zB46a10.r1 Soares fetal lung NBHL19W Homo sapiens cDNA clone 306618

DE 5'

KW EST.

OS Homo sapiens (human)

OC Eukaryotae; mitochondrion eukaryotes; Metazoa; Chordata;

OC Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP 1-161
RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
RA Parsons J., Rifkin L., Rohlfing T., Tan F., Trevaskis E.,
RA Waterston R., Williamson A., Wohlmann P., Wilson R.;
RA "WashU-Merck EST Project";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC estevenson.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Insert Length: 988 Std Error: 0.00 Seq primer:
CC mob.REGA+FT.
FH Key Location/Qualifiers
FH source
FT 1..161
FT /organism="Homo sapiens"
FT /note="Organ: lung; Vector: p7T3D (Pharmacia) with a
FT modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer
FT [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'],
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified p7T3 vector
FT (Pharmacia). Library went through one round of
FT normalization to a Cot = 5. Library constructed by Bento
FT Soares and M.Fatima Bonaldo. This library was constructed
FT from the same fetus as the fetal heart library, Soares
FT fetal heart NBH19W."
FT /clone="306618"
FT /clone_lib="Soares fetal lung NBH19W"
FT /dev_stage="19 weeks"
FT /lab_host="DH10B (ampicillin resistant)"
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FT Sequence 161 BP; 33 A; 46 C; 38 G; 44 T; 0 other;
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Query Match 7.4%; Score 154; DB 88; Length 161;
Best Local Similarity 99.4%; Pred. No. 1.68e-256;
Matches 160; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy 1063 CTCCCTCAGCTCTCTGGAGACCTCTTACCGCTGCTGCTAGCGCTGGGAGACTGATA 1122
Db 61 acttggggagggcaagagactgggagccattctcccccagaagtggttaacgggttttagc 120
Qy 1123 ACTTGGGGAGGCAAGAGACTGGGAGCCACTTCTCCCGAAGTGTTTACGGTTTACG 1182
Db 121 ttttataataaccctgtgagaagccattccaccattct 161
Qy 1183 TTTTATAATACCTGTGTGAGA-GCCCATTCGCCACCAATCT 1222
RESULT 3
ID MM1142e20 standard; RNA; EST; 133 BP.
AC AA185611;
NI 91769266
DT 21-FEB-1997 (Rel. 51, Created)
DT 22-FEB-1997 (Rel. 51, Last updated, Version 2)
DE mt62a08.r1 Soares 2NbMT Mus musculus cDNA clone 634454 5' similar
DE to TR:G595926 G595926 BAK-2 PROTEIN. ;
KW EST.
OS Mus musculus (house mouse)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-133
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,

Waterston R.;
RA "The WashU-HHMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
CC Washington University School of Medicine 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through LLNL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:386446 Trace
CC considered overall poor quality possible reversed clone; similarity
CC on wrong strand Seq primer: *28M13 rev2 from Amersham High quality
CC sequence stop: 1.
FH Key Location/Qualifiers
FH source
FT 1..133
FT /organism="Mus musculus"
FT /strain="C57BL/6J"
FT /note="Vector: p7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT was primed with a Not I - oligo(dT) primer [5'
FT TGTACCAATCTGAAGTGGAGCGCGCTTTTTTTTTTTTTTTT
FT 3']; double-stranded cDNA was ligated to Eco RI adapters
FT (Pharmacia), digested with Not I and cloned into the Not I
FT and Eco RI sites of the modified p7T3 vector. RNA provide
FT by Dr. Bertrand Jordan. Library went through two rounds of
FT normalization, and was constructed by Bento Soares and
FT M.Fatima Bonaldo."
FT /clone="634454"
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FT /sex="male"
FT /tissue_type="Thymus"
FT /dev_stage="4 weeks"
FT /lab_host="DH10B"
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FT mRNA
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SQ
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Best Local Similarity 81.6%; Pred. No. 9.33e-55;
Matches 71; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Db 41 ccgtccctcttgacagcaggttgcctatcacacagagagggttttcgaagctacgta 100
Qy 258 CCCTCTGCTCTGTGAGGACGAGTAGCCAGGAGGAGGTTTCCCGAGCTACGTT 317
Db 101 ttctacctcaccagcaggaacatgag 127
Qy 318 TTTTACCCCATCAGCAGGAACAGGAG 344
RESULT 4
LOCUS AA185611 133 bp mRNA EST 19-FEB-1997
DEFINITION mt62a08.r1 Soares 2NbMT Mus musculus cDNA clone 634454 5' similar
TO TR:G595926 G595926 BAK-2 PROTEIN. ;
ACCESSION AA185611
NID 91769266
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 133)
AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project

Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu


```

TGTACCAATCTGAAGTGGGAGCGCGCGAATCTTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo.
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/tissue_type="Liver"
/lab_host="DH10B"
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Matches 91; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

Db 198 tctctaccatccatccatcttttgcctgggctgcagctctcagggattctgagccc 257
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Qy 1417 TCCCATTCCTCCCTCCGCCATACCTGCTTGCAGTTGGACTCTCAGGGATCTGGGCTT 1476

Db 258 agagtggcagcagaggtgaggttcagaccacagctgtctgaacacatccatcaggtc- 316
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Qy 1477 GGGTGTGGGTGGGGTGGAGTCGCAGACCAGAGCTGTCTGAACCTCAGTGTTCAGAAACC 1536

Db 317 tccaatctctgtccc 331
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Qy 1537 TCCAAGCCTGCCTCC 1551

RESULT 9
LOCUS      MM1158998 standard; RNA; EST; 498 BP.
DEFINITION AA242472;
            NI 91873149
DT 11-MAR-1997 (Rel. 51, Created)
DT 11-MAR-1997 (Rel. 51, Last updated, Version 1)
DE mx26g11.r1 Soares mouse NML Mus musculus cDNA clone 681380 5'.
KW EST.
OS Mus musculus (house mouse)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-498
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RA "The WashU-HHMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
CC Washington University School of Medicine 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through LLNL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:421084 Seq
CC primer: -28m13 rev2 ET from Amersham High quality sequence stop:
CC 477.
FH Key      Location/Qualifiers
FH 1..498
FT source
FT /organism="Mus musculus"
FT /note="vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT was primed with a Not I - oligo(dT) primer [5'
FT TGTACCAATCTGAAGTGGGAGCGCGCGAATCTTTTTTTTTTTTTTTT 3']";
FT double-stranded cDNA was ligated to Eco RI adaptors
FT (Pharmacia), digested with Not I and cloned into the Not I
FT and Eco RI sites of the modified pT73 vector. Library
FT constructed and normalized by Bento Soares and M.Fatima
FT Bonaldo."

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FT /clone_lib="Soares mouse NML"
FT /tissue_type="Liver"
FT /lab_host="DH10B"
FT mRNA
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Best Local Similarity 67.4%; Pred. No. 7.47e-32;
Matches 91; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

Db 198 tctctaccatccatccatcttttgcctgggctgcagctctcagggattctgagccc 257
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Qy 1417 TCCCATTCCTCCCTCCGCCATACCTGCTTGCAGTTGGACTCTCAGGGATCTGGGCTT 1476

Db 258 agagtggcagcagaggtgaggttcagaccacagctgtctgaacacatccatcaggtc- 316
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Qy 1477 GGGTGTGGGTGGGGTGGAGTCGCAGACCAGAGCTGTCTGAACCTCAGTGTTCAGAAACC 1536

Db 317 tccaatctctgtccc 331
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Qy 1537 TCCAAGCCTGCCTCC 1551

RESULT 10
LOCUS      AA123834 310 bp mRNA EST 21-NOV-1996
DEFINITION mp93c04.r1 Soares 2NDMT Mus musculus cDNA clone 576774 5' similar
            to TR:G595926 G595926 BAK-2 PROTEIN. ;.
ACCESSION  AA123834
NID        91682242
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Mus.
REFERENCE  1 (bases 1 to 310)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HHMI Mouse EST Project
            Unpublished (1996)
TITLE     Contact: Marra M/Mouse EST Project
JOURNAL   WashU-HHMI Mouse EST Project
COMMENT   Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:351422
            Seq primer: -28m13 rev2 from Amersham.
            Location/Qualifiers
            1..310
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /note="vector: pT73D-Pac (Pharmacia) with a modified
            polylinker; Site_1: Not I; Site_2: Eco RI; [5'
            TGTACCAATCTGAAGTGGGAGCGCGCGGTTTTTTTTTTTTTTTTTTTTTTTTT
            3']; double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not
            I and Eco RI sites of the modified pT73 vector. RNA
            provided by Dr. Bertrand Jordan. Library went through two
            rounds of normalization, and was constructed by Bento
            Soares and M.Fatima Bonaldo."
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FEATURES
source

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ORIGIN

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Best Local Similarity 78.2%; Pred. No. 1.60e-28;
Matches 104; Conservative 0; Mismatches 22; Indels 7; Gaps 5;

Db 195 ctcacacagacctgaaatggcatctggacaaaggaccaggtcccccgaagtgggc-tg 243
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Qy 182 CTCCTACTGAGACCTGAAATATGGCTTCGGGCAAGGCCAGGTCTCTCCAGGAGGAGTG 241
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Db 244 cgaatgagtc--ccc-gtcc-c--cttctgaacagcaggttgcacagacacagaggaagt 297
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Qy 242 CGGAGAGCCTGCCCTGCTCTGCTTCTGAGAGCAGGTAGCCCGGACACAGAGGAGGT 301
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Db 298 ctttcgaagctac 310
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Qy 302 TTCCGCAGCTAC 314

RESULT 11
ID MAA23834 standard; RNA; EST; 310 BP.
AC AA123834;
NI G1682242;
DT 25-NOV-1996 (Rel. 50, Created)
DE 19-FEB-1997 (Rel. 51, Last updated, Version 2)
DE mp93c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
DE to TR:G595926 G595926 BAK-2 PROTEIN. ;
KW EST.
OS Mus musculus (house mouse)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-310
RA Maria M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisler S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RA "The WashU-HHMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
CC Washington University School of MedicineP 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.wustl.edu This clone is available
CC royalty-free through LNL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:351422 Seq
CC primer: -28M13 rev2 from Amersham.
FH Key
FH Location/Qualifiers
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FT 1..310
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FT /strain="C57BL/6J"
FT /note="vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
FT was primed with a Not I - oligo(dT) primer [5',
FT TGTTCACATCTGAAGTGGGAGCGCGCGTCTTTTCTTTTCTTTTCTTTTCTTTT
FT 3']; double-stranded cDNA was ligated to Eco RI adaptors
FT (Pharmacia), digested with Not I and cloned into the Not I
FT and Eco RI sites of the modified pT7T3 vector. RNA provide
FT by Dr. Bertrand Jordan. Library went through two rounds of
FT normalization, and was constructed by Bento Soares and
FT M.Fatima Bonaldo."
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FT /clone_lib="Soares 2NbMT"
FT /sex="male"
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FT /dev_stage="4 weeks"
FT /lab_host="DH10B"
FT mRNA

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Best Local Similarity 78.2%; Pred. No. 1.60e-28;
Matches 104; Conservative 0; Mismatches 22; Indels 7; Gaps 5;

Db 185 ctcacacagacctgaaatggcatctggacaaaggaccaggtcccccgaagtgggc-tg 243
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Qy 182 CTCCTACTGAGACCTGAAATATGGCTTCGGGCAAGGCCAGGTCTCTCCAGGAGGAGTG 241
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Db 244 cgaatgagtc--ccc-gtcc-c--cttctgaacagcaggttgcacagacacagaggaagt 297
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Qy 242 CGGAGAGCCTGCCCTGCTCTGCTTCTGAGAGCAGGTAGCCCGGACACAGAGGAGGT 301
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Db 298 ctttcgaagctac 310
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Qy 302 TTCCGCAGCTAC 314

RESULT 12
LOCUS      AA123834      310 bp      mRNA      EST      17-FEB-1997
DEFINITION mp93c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;
ACCESSION      AA123834
NID      G1682242
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE      1 (bases 1 to 310)
AUTHORS      Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
      Geisler S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
      Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
      Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
      Waterston R.
TITLE      The WashU-HHMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
      WashU-HHMI Mouse EST Project
      Washington University School of MedicineP
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: mouseest@wustl.wustl.edu
      This clone is available royalty-free through LNL; contact the
      IMAGE Consortium (info@image.llnl.gov) for further information.
      MGI:351422
      Seq primer: -28M13 rev2 from Amersham.
      Location/Qualifiers
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      /organism="Mus musculus"
      /strain="C57BL/6J"
      /note="vector: pT7T3D-Pac (Pharmacia) with a modified
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      was primed with a Not I - oligo(dT) primer [5',
      TGTTCACATCTGAAGTGGGAGCGCGCGTCTTTTCTTTTCTTTTCTTTTCTTTT
      3']; double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT7T3 vector. RNA
      provided by Dr. Bertrand Jordan. Library went through two
      rounds of normalization, and was constructed by Bento
      Soares and M.Fatima Bonaldo."
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QY 182 CTCCACTGAGACCTGAAAATGGCTTCGGGCAAGGCCAGGTCTCCAGGACGAGGTG 241

Db 244 cgatgagtc--ccc-gtcc-c--cttcgaacacagcaggttccccagacacagagaggt 297
QY 242 CGAGAGCGCTGCCCTGCTCTGCTTCTGAGGACGAGGTAGCCAGGACACAGAGGAGGT 301

Db 298 ctttcgaagctac 310
QY 302 TTTCGCGAGCTAC 314

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LOCUS      AAL139013          320 bp      mRNA          EST          16-FEB-1997
DEFINITION mr04a06.r1 Soares mouse 3NDMS Mus musculus cDNA clone 596434 5'
similar to TR:G595926 G595926 BAK-2 PROTEIN. ;.
ACCESSION  AAL139013
NID        91701240
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus.
            Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Mus.

REFERENCE  1 (bases 1 to 320)
AUTHORS   Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
            Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
            Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
            Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
            Waterston R.
            The WashU-HHMI Mouse EST Project
            Unpublished (1996)

TITLE     The WashU-HHMI Mouse EST Project
JOURNAL
COMMENT   Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:361866
            Seq primer: -28M13 rev2 from Amer sham.
            Location/Qualifiers
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                TGTACCAATCTGAAGTGGGAGCGCGCGCTGTCTTTTCTTTTCTTTTCTTTT
                3']; double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. RNA
                provided by Dr. Bertrand Jordan. Library went through
                three rounds of normalization, and was constructed by
                Bento Soares and M.Fatima Bonaldo."
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                /tissue_type="Spleen"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
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FEATURES
source
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/strain="FVB/N"
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polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGCGCTGTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[GTGGAATCGGTACC], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."
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/clone_lib="Barstead mouse pooled organs MRLRB4"
/sex="mixed"
/dev_stage="7 day"
/lab_host="DH10B"
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SQ Sequence 331 bp; 78 A; 104 C; 89 G; 60 T; 0 other;

Query Match      1.9%; Score 39; DB 108; Length 331;
Best Local Similarity 84.2%; Pred. No. 6.98e-27;
Matches 48; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 275 ccgtccctctctgaacacaggttccccagacacagaggttcttcgaagctac 331
QY 258 CCCTCTGCTTCTGAGGACGAGGTAGCCAGGACACAGAGGAGGTTCCTCCGAGCTAC 314

RESULT 15
LOCUS      AA220617          331 bp      mRNA          EST          10-FEB-1997

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Search completed: Thu Aug 21 11:52:14 1997
Job time : 1336 secs.

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(TM)

CONFIDENTIAL

Result No.	Query			DB	ID	Description	Pred. No.
	Score	Match	Length				
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2	1561	100.0	211	17	R14451	Bcl-2 protein.	5.68e-137
3	1561	100.0	211	13	R77876	Human Cdn-1.	5.68e-137
4	1529	98.0	211	20	W03669	Bak-2 protein.	7.28e-134
5	1529	98.0	211	13	R77877	Human Cdn-2.	7.28e-134
6	1154	73.9	152	13	R77879	Human Cdn-1(60-211).	1.48e-97
7	1079	69.1	141	13	R77880	Human Cdn-1(71-211).	2.53e-90
8	898	57.5	116	13	R77881	Human Cdn-1(96-211).	6.25e-73
9	272	17.6	190	13	R68884	Chicken lymphoid BCL-2.	1.74e-14
10	272	17.4	232	19	W01020	Apoptosis-blocking pr	2.62e-14
11	266	17.0	233	13	R68887	Human thymus BCL-XL.	8.94e-14
12	266	17.0	233	20	W05821	Bcl-XL protein.	8.94e-14
13	261	16.7	232	19	W01019	Apoptosis-blocking pr	2.48e-13
14	261	16.7	239	19	W01018	Apoptosis-blocking pr	2.48e-13
15	259	16.6	205	13	R17405	Human bcl-2 beta prot	3.72e-13
16	259	16.6	205	13	R68886	Human thymus BCL-2.	3.72e-13
17	259	16.6	205	13	R70332	Human bcl-2 protein.	3.72e-13
18	259	16.6	239	13	R17404	Human bcl-2 alpha pro	3.72e-13
19	259	16.6	239	9	R47344	Human oncogene bcl-2	3.72e-13
20	259	16.6	239	1	R09878	Sequence of bcl-2-alp	3.72e-13

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1  MASGGGPPPRQECGEPALPSAEQVAQDTTEEFVRSYFYRRHQCEAGVAAPDP 60

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Db 61 vtllpqpstmgvgrqlaigddinnrydsefqtmiqlhqlptaenayeyftkiatslfe 120
 QY 61 vtllpqpstmgvgrqlaigddinnrydsefqtmiqlhqlptaenayeyftkiatslfe 120
 Db 121 sginwgrvllgfyrlalhvyghltgflgqtrfvvdfmlhchlarwiagrgwvaa 180
 QY 121 sginwgrvllgfyrlalhvyghltgflgqtrfvvdfmlhchlarwiagrgwvaa 180
 Db 181 lnlgngpnlvllgvllgqfvvrrffks 211
 QY 181 lnlgngpnlvllgvllgqfvvrrffks 211

RESULT 2

ID R81451 standard; Protein; 211 AA.
 AC R81451;
 DT 02-JUL-1996 (first entry)
 DE Bcl-2 apoptosis-related protein.
 KW Bcl-2; apoptosis; cell proliferation; cell death; diagnosis;
 KW therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 188..205
 FT /note= "putative membrane localisation sequence"
 FT /label= C-terminal_domain
 PN WO9605232-A1.
 PD 22-FEB-1996.
 PF 09-AUG-1995; U10103.
 PR 09-AUG-1994; US-287427.
 PR 11-OCT-1994; US-321071.
 PA (IMMUNO-) IMMUNOGEN INC.
 PI Chittenden TD;
 DR WPI: 96-139648/14.
 DR N-PSDB: T17375.
 PT New isolated human Bcl-2 protein - used to develop prods. for
 PT treating disorders characterised by inappropriate cell proliferation
 PT or cell death
 PS Claim 3; Fig 4; 100pp; English.
 CC Bcl-2 protein (R81451) is a member of the Bcl-2 family and can
 CC induce apoptosis in cells and function as a negative regulator of
 CC lines examined. Bcl-2 mRNA was detected in all human tumour cell
 CC tissues. It can be obtained by expression of a full-length cDNA
 CC clone (T17375) in pref. mammalian host cells. Bcl-2 can be used to
 CC develop prods. for treating disorders associated with inappropriate
 CC cell proliferation or cell death, and to raise antibodies used for
 CC the diagnosis or monitoring of such disorders.
 SQ Sequence 211 AA;

Query Match 100.0%; Score 1561; DB 17; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5,68e-137;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 masgggppprqecgepalpsaseeqvaqtteevfrsyvyrhqqeaeagvaapadp 60
 QY 1 MASGGGPPPRQECGEPAIPSAEEQVAQDTEEVFRSYVYRHHQEQEAEAGVAAPADPEM 60
 Db 61 vtllpqpstmgvgrqlaigddinnrydsefqtmiqlhqlptaenayeyftkiatslfe 120
 QY 61 vtllpqpstmgvgrqlaigddinnrydsefqtmiqlhqlptaenayeyftkiatslfe 120
 Db 121 sginwgrvllgfyrlalhvyghltgflgqtrfvvdfmlhchlarwiagrgwvaa 180
 QY 121 sginwgrvllgfyrlalhvyghltgflgqtrfvvdfmlhchlarwiagrgwvaa 180
 Db 181 lnlgngpnlvllgvllgqfvvrrffks 211
 QY 181 lnlgngpnlvllgvllgqfvvrrffks 211

RESULT 3

ID R77876 standard; Protein; 211 AA.
 AC R77876;

DT 21-NOV-1995 (first entry)
 DE Human Cdn-1.
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN WO9515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 95-215106/28.
 DR N-PSDB: Q95492.
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure: Fig. 3A-B: 66pp; English.
 CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
 CC previously isolated clone as probe. Recombinant Cdn-1 was produced
 CC in Sf9 and human colon adenocarcinoma HT29 cells. Expression of
 CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
 CC survival in response to anti-Fas-mediated apoptosis.
 SQ Sequence 211 AA;

Query Match 100.0%; Score 1561; DB 13; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5,68e-137;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 masgggppprqecgepalpsaseeqvaqtteevfrsyvyrhqqeaeagvaapadp 60
 QY 1 MASGGGPPPRQECGEPAIPSAEEQVAQDTEEVFRSYVYRHHQEQEAEAGVAAPADPEM 60
 Db 61 vtllpqpstmgvgrqlaigddinnrydsefqtmiqlhqlptaenayeyftkiatslfe 120
 QY 61 vtllpqpstmgvgrqlaigddinnrydsefqtmiqlhqlptaenayeyftkiatslfe 120
 Db 121 sginwgrvllgfyrlalhvyghltgflgqtrfvvdfmlhchlarwiagrgwvaa 180
 QY 121 sginwgrvllgfyrlalhvyghltgflgqtrfvvdfmlhchlarwiagrgwvaa 180
 Db 181 lnlgngpnlvllgvllgqfvvrrffks 211
 QY 181 lnlgngpnlvllgvllgqfvvrrffks 211

RESULT 4

ID W03669 standard; Protein; 211 AA.

AC W03669;
 DT 22-FEB-1997 (first entry)
 DE Bak-2 protein.
 KW Human; Bak-2; apoptosis; latency; virus replication;
 KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.
 OS Homo sapiens.
 PN WO9633416-A1.
 PD 24-OCT-1996.
 PF 19-APR-1996; U05639.
 PR 20-APR-1995; US-426529.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 96-485886/48.
 DR N-PSDB: T42139.
 PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 PS Disclosure: Fig 2; 24pp; English.
 CC This Bak-2 protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
 CC protein, and is capable of modulating apoptosis. The protein may

CC be used in complete or partial form, or as an epitope tag fusion
 CC protein, in a new virucide drug screening method, which involves
 CC combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),
 CC exposure to a test compound, and monitoring for disruption of the
 CC interaction, e.g. by co-precipitation, protein interactive trapping
 CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
 CC replication or latency in the absence of apoptosis. Compounds which
 CC inhibit the interaction may be used as virucide, antitumour or
 CC diagnostic agents.
 SQ Sequence 211 AA;

Query Match 98.0%; Score 1529; DB 20; Length 211;
 Best Local Similarity 97.2%; Pred. No. 7, 28e-134;
 Matches 205; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 masgggppprqecgepalpaseeqvaqdtteevfrsyfhhqgeaeagaapadpem 60
 Qy 1 MASGGGPPPRQECGEPAIPASAEQVAQDTTEEVFRSYFHHQGEAEAGAAPADPEM 60

Db 61 vtllpqsstmgqgrqlaigddinnrydsfqtmlqhlqptaeayeyftkiasslfe 120
 Qy 61 VTLLPQSSSTMGGQGRQLAIGDDINNRYDSEFQTMQLQHLQPTAEAYEYFTKIATSLFE 120

Db 121 sginwgrvvalgfysrlalhiygrlgtflgqvtrfvdfmlhchciarwiagrgwvaa 180
 Qy 121 SGINWGRVVALGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHCHCIARWIAQRGGWVA 180

Db 181 lnlngpnlvvlvlgvllgqfvrrffks 211
 Qy 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 5

ID R77877 standard; Protein; 211 AA.
 AC R77877;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-2.
 KW Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN W09515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI; 95-215106/28.
 DR N-PSDB; Q95493.
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure; Fig.5D-E; 66pp; English.
 CC Cdn-2 cDNA was isolated from a human placental genomic library
 CC using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
 CC in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced
 CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
 CC with Cdn-1 (R77876).
 SQ Sequence 211 AA;

Query Match 98.0%; Score 1529; DB 13; Length 211;
 Best Local Similarity 97.2%; Pred. No. 7, 28e-134;
 Matches 205; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 masgggppprqecgepalpaseeqvaqdtteevfrsyfhhqgeaeagaapadpem 60
 Qy 1 MASGGGPPPRQECGEPAIPASAEQVAQDTTEEVFRSYFHHQGEAEAGAAPADPEM 60

Db 61 vtllpqsstmgqgrqlaigddinnrydsfqtmlqhlqptaeayeyftkiasslfe 120
 Qy 61 VTLLPQSSSTMGGQGRQLAIGDDINNRYDSEFQTMQLQHLQPTAEAYEYFTKIATSLFE 120

Db 121 sginwgrvvalgfysrlalhiygrlgtflgqvtrfvdfmlhchciarwiagrgwvaa 180
 Qy 121 SGINWGRVVALGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHCHCIARWIAQRGGWVA 180

Db 181 lnlngpnlvvlvlgvllgqfvrrffks 211
 Qy 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 6

ID R77879 standard; Protein; 152 AA.
 AC R77879;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-1(60-211).
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN W09515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI; 95-215106/28.
 DR New nucleic acid sequences encoding Cdn apoptosis modulators - and
 DR related vectors, transformed cells, proteins and antibodies, useful
 DR or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 DR etc.
 PS Disclosure; Fig.11; 66pp; English.
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
 CC decreased this activity, suggesting that small, truncated Cdn-1
 CC molecules may be potent therapeutics.
 SQ Sequence 152 AA;

Query Match 73.9%; Score 1154; DB 13; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1, 48e-97;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvtlplqpsstmgqgrqlaigddinnrydsfqtmlqhlqptaeayeyftkiatslf 60
 Qy 60 MVTLPQPSSTMGQGRQLAIGDDINNRYDSEFQTMQLQHLQPTAEAYEYFTKIATSLF 119

Db 61 esginwgrvvalgfysrlalhiygrlgtflgqvtrfvdfmlhchciarwiagrgwvaa 120
 Qy 120 ESGINWGRVVALGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHCHCIARWIAQRGGWVA 179

Db 121 alnlngpnlvvlvlgvllgqfvrrffks 152
 Qy 180 ALNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 7

ID R77880 standard; Protein; 141 AA.
 AC R77880;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-1(71-211).
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN W09515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI; 95-215106/28.

DT 30-MAR-1997 (first entry)

PA (UYSL-) UNIV ST LOUIS.

PI Chinnadurai G;
 DR WPI; 96-427055/43.
 PT Nucleic acids encoding apoptosis regulating proteins - useful for
 PS diagnosing and treating immune disorders, malignancies, etc.
 CC Example 8; Page 33-34; 60pp; English.
 CC The 42-8 mutant (W01019) of the Bcl-2 oncogene product (W01018)
 CC lacks amino acids 42-48 of the native protein. This and other
 CC Bcl-2 mutants (see also W01020-21) were used in a two hybrid assay
 CC to examine the interactions between Bcl-2 and novel apoptosis-
 CC regulating proteins Nip1, Nip2 and Nip3 (W00997-99). The Nip
 CC proteins were unable to interact with mutant 42-8. The site of
 CC deletion in this mutant corresponds to a motif (see also W01003)
 CC on Bcl-2 essential for interaction with Nip proteins. A second
 CC binding motif (W01004) of Bcl-2 was also identified, and both
 CC show homology to motifs (W01005-06) found on the 19K protein
 CC (W01010) of adenovirus ElB.
 SQ Sequence 232 AA;

Query Match 16.7%; Score 261; DB 19; Length 232;
 Best Local Similarity 29.3%; Pred. No. 2.48e-13;
 Matches 41; Conservative 37; Mismatches 57; Indels 5; Gaps 4;

Db 67 tpaagaaagpalapvpvvhlt--lrqagddfrryrrdfaemssqlhltpftargcfa 124
 Qy 54 APADPEMVTLP-LQPSTMGQVGRQLAIGDDINRRYDSEFTMLQLHPTAENAYEFT 112
 Db 125 tvveelfrdgwngrivaffefggvmcvesvnrmsplvndialwmtteylnrh-lhtwiq 183
 Qy 113 KIATSLFESGINMGWRVALLGFGYRLALHVYQHGLTGFLGQVTRFVDFMLHHCIARWIA 172
 Db 184 dnggdwafvel-ygpsmrpl 202
 Qy 173 QRGGWAAALNLGNPILNL 192

RESULT 14
 ID W01018 standard; Protein; 239 AA.
 AC W01018;
 DT 18-DEC-1996 (first entry)
 DE Apoptosis-blocking protein Bcl-2.
 KW Apoptosis-regulating protein; Bcl-2; oncogene;
 KW adenovirus ElB 19K protein; cell death; cancer; tumour;
 KW immune disorder; diagnosis; therapy; Bp1A; Bp13; Bp5; Nip1;
 KW Nip2; Nip3.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Binding_site 43..51
 FT /label= Binding_motif
 FT /note= "Interacts with Bip proteins"
 FT Binding_site 106..112
 FT /label= Binding_motif
 FT /note= "Interacts with Bip proteins"
 FT EP-733706-A2.
 PD 25-SEP-1996.
 PF 21-MAR-1996; 104542.
 PR 21-MAR-1995; US-408095.
 PA (UNIV) UNIV ST LOUIS.
 PI Chinnadurai G;
 DR WPI; 96-427055/43.
 PT Nucleic acids encoding apoptosis regulating proteins - useful for
 PT diagnosing and treating immune disorders, malignancies, etc.
 PS Example 8; Page 32-33; 60pp; English.
 CC The bcl-2 oncogene product (W01018) enhances the survival of
 CC haematopoietic B and T cells by blocking apoptosis induced by
 CC diverse agents. Its activity is similar to that of the 19K
 CC protein (W01010) of adenovirus ElB. 3 Novel proteins, Bp1A,
 CC Bp13 and Bp5 (W01000-02), that specifically interact with
 CC Bcl-2, have been identified. Mutational analysis (see also
 CC W01019-21) shows the apoptosis-regulating Nip proteins (see also
 CC W00997-99) associate with Bcl-2 at specific sites (see also
 CC W01003-04) that show homology to motifs (W01005-06) on 19K.
 SQ Sequence 239 AA;

Query Match 16.7%; Score 261; DB 19; Length 239;
 Best Local Similarity 29.3%; Pred. No. 2.48e-13;
 Matches 41; Conservative 37; Mismatches 57; Indels 5; Gaps 4;

Db 74 tpaagaaagpalapvpvvhlt--lrqagddfrryrrdfaemssqlhltpftargcfa 131
 Qy 54 APADPEMVTLP-LQPSTMGQVGRQLAIGDDINRRYDSEFTMLQLHPTAENAYEFT 112
 Db 132 tvveelfrdgwngrivaffefggvmcvesvnrmsplvndialwmtteylnrh-lhtwiq 190
 Qy 113 KIATSLFESGINMGWRVALLGFGYRLALHVYQHGLTGFLGQVTRFVDFMLHHCIARWIA 172
 Db 191 dnggdwafvel-ygpsmrpl 209
 Qy 173 QRGGWAAALNLGNPILNL 192

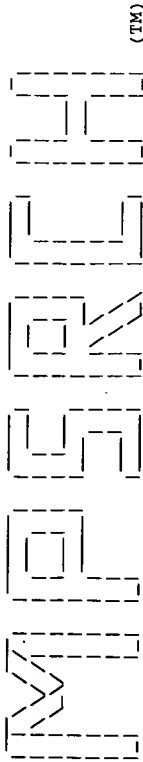
RESULT 15
 ID R71405 standard; protein; 205 AA.
 AC R71405;
 DT 30-OCT-1995 (first entry)
 DE Human bcl-2 beta protein.
 KW Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KW proliferation; cell cycle progression; Bax; apoptotic cell death;
 KW apoptosis; cytokine; death repressor; BHI; BH2; cancer therapy;
 KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
 KW ischaemic cell death.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 136..155
 FT /label= BH1_domain
 FT /note= "Represents Bax binding site"
 FT Domain 187..192
 FT /label= BH2_domain
 FT /note= "Represents Bax binding site"
 FT W09505750-A.
 PD 02-MAR-1995.
 PF 24-AUG-1994; U09701.
 PR 26-AUG-1993; US-112208.
 PR 25-MAY-1994; US-248819.
 PA (UNIV) UNIV WASHINGTON.
 PI Korsmeyer SJ;
 DR WPI; 95-106605/14.
 PT Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.
 PS Disclosure; Page 40; 139pp; English.
 CC The sequences given in R71404-05 represent the human bcl-2 alpha and
 CC beta proteins respectively. bcl-2 is encoded by a proto-oncogene and
 CC is capable of inhibiting apoptosis in many hematopoietic cell systems.
 CC bcl-2 is a 26 kD membrane-associated cytoplasmic protein and is thought
 CC to function by enhancing the survival of hematopoietic cells of B and T
 CC origins rather than directly promoting proliferation of these cell
 CC types. bcl-2 has not been shown to directly promote cell cycle
 CC progression nor does it necessarily alter the dose response to limiting
 CC concentrations of IL-3. bcl-2 has been shown to form heterodimers with
 CC a 21 kD protein, Bax. Overexpressed Bax accelerates apoptotic cell death
 CC also acts to counter the death repressor activity of bcl-2. Therefore,
 CC the ratio between bcl-2 and Bax determines cell survival or death
 CC following an apoptotic stimulus. The invention gives a mutant form of
 CC bcl-2 in which there is at least one amino acid substitution or deletion
 CC in the BH1 or BH2 domains. This makes the mutant protein substantially
 CC incapable of binding Bax and/or incapable of death repressor activity.
 CC Down regulation of bcl-2 is useful in cancer therapy, controlling
 CC hyperplasias and eliminating self-reactive clones in autoimmune by
 CC favouring death effector molecules. Up regulating bcl-2 is beneficial in
 CC treatment and diagnosis of immunodeficiency diseases, including AIDS and
 CC neurodegenerative and ischaemic cell death.
 SQ Sequence 205 AA;

Query Match 16.6%; Score 259; DB 13; Length 205;
 Best Local Similarity 29.7%; Pred. No. 3.72e-13;

	Matches	38;	Conservative	37;	Mismatches	49;	Indels	4;	Gaps	3;
Db	74	tpaapgaagpalsppvpvhl	--lrqagddfsrryrgd	faemssqlhltpftargfa	131					
Qy	54	APADPEMVTLP-LQPSSTM	QVGRQLAIIGDDINRRYD	SEFQTMQLQLQPTAENAYEYFT	112					
Db	132	tvveelfrdgvnwgrivaf	feffgvmcvesvnr	emspdvdnialwmt	eylorh-lhtwiq	190				
Qy	113	KIATSLFESGINWGRVVAL	LGFGYRLALHVYQHGLTG	FLGQYTRFVVDFMLHHC	IARWIA	172				
Db	191	dnnggwga	198							
Qy	173	QGGWVA	180							

Search completed: Wed Aug 20 11:00:33 1997
 Job time : 45 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Aug 20 11:00:51 1997; MasPar time 8.88 Seconds

Tabular output not generated. 686.301 Million cell updates/sec

Title: >US-08-320-157-7

Description: (1-211) from US08320157.pap

Perfect Score: 1561

Sequence: 1 MASCGGPGPRQECGEALP.....LVILGVLLGQFVVRFFKS 211

Scoring table: PAM 150
Gap 11

Searched: 91006 seqs, 28888923 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir51

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann16:unrev

Statistics: Mean 45.149; Variance 108.206; scale 0.417

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1561	100.0	211	13	Bak protein - human	4.94e-244
2	1529	98.0	211	13	cdn-2 protein - huma	2.15e-238
3	274	17.6	190	13	apoptosis regulator	3.11e-24
4	270	17.3	233	14	BCL-X protein - rat	1.27e-23
5	270	17.3	233	14	bcl-x long - mouse	1.27e-23
6	266	17.0	233	13	apoptosis regulator	5.19e-23
7	263	16.8	214	14	bcl-x transmembrane	1.49e-22
8	262	16.8	216	6	transforming protein	2.11e-22
9	261	16.7	233	6	transforming protein	2.99e-22
10	259	16.6	205	2	transforming protein	6.01e-22
11	255	16.3	206	6	transforming protein	2.43e-21
12	255	16.3	239	2	transforming protein	2.43e-21
13	252	16.1	233	14	BCL-X-long - rat	6.88e-21
14	250	16.0	199	2	transforming protein	1.38e-20
15	250	16.0	236	2	transforming protein	1.38e-20
16	250	16.0	237	6	transforming protein	1.38e-20
17	247	15.8	232	14	BCL-2 - rat (fragmen	3.89e-20
18	239	15.3	232	6	transforming protein	6.14e-19
19	217	13.9	192	14	programmed cell deat	1.09e-15
20	206	13.2	192	13	bcl-2-associated pro	4.28e-14
21	201	12.9	218	13	bcl-2-associated pro	2.24e-13

22	192	12.3	350	13	A47476	BCL2 homolog MCL1 -	4.28e-12
23	186	11.9	133	14	I53295	bax - rat (fragment)	3.00e-11
24	183	11.7	154	14	I58194	gene bcl-2 protein -	7.87e-11
25	177	11.3	143	13	I38921	BAX splice form delt	5.36e-10
26	176	11.3	172	14	I49449	hemopoietic-specific	7.37e-10
27	114	7.3	890	8	S44150	coat protein - straw	6.55e-02
28	112	7.2	255	5	S26032	cytochrome-c oxidase	1.11e-01
29	111	7.1	177	13	S54778	NR-13 protein - quai	1.44e-01
30	107	6.9	400	10	S35958	beta-glucosidase - S	4.07e-01
31	107	6.9	470	2	SYPSRA	threonine synthase (4.07e-01
32	106	6.8	133	4	GPBPp4	gop protein - satell	5.25e-01
33	100	6.4	560	7	S46724	hexose transport pro	2.35e-00
34	100	6.4	567	7	S31294	hexose transport pro	2.35e-00
35	100	6.4	567	11	I70110	HXT3 protein - yeast	2.35e-00
36	97	6.2	170	14	I49055	bcl-x short - mouse	4.88e-00
37	97	6.2	814	1	CZCLEM	cellulase (EC 3.2.1.	4.88e-00
38	95	6.1	206	11	B28443	phosphatidyl-N-methy	7.87e-00
39	95	6.1	471	7	A39024	collagen alpha 3(IV)	7.87e-00
40	96	6.1	527	16	S62484	hypothetical protein	6.20e-00
41	95	6.1	532	16	S65787	glutamyl-trna synth	7.87e-00
42	95	6.1	569	7	S50771	sugar transport prot	7.87e-00
43	95	6.1	817	1	RRVGT	RNA-directed RNA pol	7.87e-00
44	95	6.1	885	11	S22389	acetylglutamate kina	7.87e-00
45	96	6.1	2007	3	B43402	myosin heavy chain-B	6.20e-00

ALIGNMENTS

RESULT	1	S58873	#type complete
ENTRY		Bak protein - human	
TITLE		bcl-2 homolog; cdn-1 protein	
ALTERNATE_NAMES		#formal_name Homo sapiens #common_name man	
ORGANISM		15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change	
DATE		06-Sep-1996	
ACCESSIONS		S58873; S58872; S58874	
REFERENCE		S58873	
#authors		Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I.; Guild, B.C.	
#journal		Nature (1995) 374:733-736	
#title		Induction of apoptosis by the Bcl-2 homologue Bak.	
#accession		S58873	
##status		preliminary; nucleic acid sequence not shown	
##molecule_type		mrna	
##residues		1-211 #label CHI	
##cross-references		EMBL:U23765	
REFERENCE		S58872	
#authors		Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martinou, J.C.; Brown, R.	
#journal		Nature (1995) 374:731-733	
#title		Cloning of a bcl-2 homologue by interaction with adenovirus	
#accession		S58872	
##status		preliminary	
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##cross-references		EMBL:X84213	
REFERENCE		S58874	
#authors		Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, P.J.	
#journal		Nature (1995) 374:736-739	
#title		Modulation of apoptosis by the widely distributed Bcl-2	
#accession		S58874	
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GENETICS			
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##cross-references		GDB:635887	
SUMMARY		#length 211 #molecular-weight 23409 #checksum 801	


```

5
RESULT 5
ENTRY bcl-x long - mouse
TITLE bcl-x long - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
15-Oct-1996
ACCESSION I49056 #type complete
REFERENCE I49055
#authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in B
and T lymphocytes.
#cross-references MUID:95052604
#accession I49056
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-233 #label RES
#cross-references EMBL:U10101; NID:g506647; CDS_PID:g506648
REFERENCE S52866
#authors Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
#submission submitted to the EMBL Data Library, November 1994
#description IL-5 inhibits anti-IgM-induced apoptosis in an immature B
cell line through induction of bcl-xL.
#accession S52866
#status preliminary
#molecule_type mRNA
#residues 1-233 #label KAM
#cross-references EMBL:X83574
SUMMARY #length 233 #molecular-weight 26132 #checksum 5739

Query Match 17.3%; Score 270; DB 14; Length 233;
Best Local Similarity 25.5%; Pred. No. 1.27e-23;
Matches 36; Conservative 42; Mismatches 60; Indels 3; Gaps 3;

Db 61 dspavngatghs-ssldarevipmaavkqalreagdefelrlyrrafsdltsqhlhpgta 119
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 48 EAEgVAAPADPEMVTLPQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMLOHLQPTAENA 107
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 ygsfeqvnnelfrdgvnwgrivaffsgalcvsvdkemqvlsvraswmatylnhdh-1 178
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 108 YEFTKIATSLFESGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHC1 167
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 epwiqenggdwtdfvlvgnna 199
||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 168 ARWIAQRGGWVAALNL-GNGP 187

RESULT 6
ENTRY bcl-2 related protein
TITLE bcl-2 related protein
ALTERNATE_NAMES bcl-xL - human
CONTAINS bcl-2-related protein
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
06-Sep-1996
ACCESSION B47537
REFERENCE B47537
#authors Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turkaz, L.A.; Mao, X.; Nunez, G.; Thompson,
C.B.
#journal Cell (1993) 74:597-608
#title bcl-x, a bcl-2-related gene that functions as a dominant
regulator of apoptotic cell death.
#accession B47537
#status nucleic acid sequence not shown; translated from
GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-233 #label BOI
#cross-references GB:L20121; CDS_PID:Q07817
#accession C47537
#status nucleic acid sequence not shown; translated from
GB/EMBL/DBJ

```

```

#molecule_type mRNA
#residues 1-69, 'G', 71-125, 189-233 ##label B02
#cross-references GB:L20122; CDS_PID:g623237
GENETICS
#gene GDB:BCL2L
#cross-references GDB:228079
KEYWORDS alternative splicing; apoptosis
FEATURE
1-233 #product apoptosis regulator bcl-xL #status predicted
#label MAT\
1-125, 189-233 #product apoptosis regulator bcl-xS #status predicted
#label MA2
SUMMARY #length 233 #molecular-weight 26063 #checksum 5340

Query Match 17.0%; Score 266; DB 13; Length 233;
Best Local Similarity 25.5%; Pred. No. 5.19e-23;
Matches 36; Conservative 42; Mismatches 60; Indels 3; Gaps 3;

Db 61 dspavngatghs-ssldarevipmaavkqalreagdefelrlyrrafsdltsqhlhpgta 119
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 48 EAEgVAAPADPEMVTLPQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMLOHLQPTAENA 107
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 ygsfeqvnnelfrdgvnwgrivaffsgalcvsvdkemqvlsvraswmatylnhdh-1 178
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 108 YEFTKIATSLFESGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHC1 167
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 epwiqenggdwtdfvlvgnna 199
||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 168 ARWIAQRGGWVAALNL-GNGP 187

RESULT 7
ENTRY bcl-x transmembrane deleted - mouse
TITLE bcl-x transmembrane deleted - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSION I49057
REFERENCE I49055
#authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in B
and T lymphocytes.
#cross-references MUID:95052604
#accession I49057
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-214 #label RES
#cross-references EMBL:U10102; NID:g506649; CDS_PID:g506650
GENETICS
#note gene name bcl-x long
SUMMARY #length 214 #molecular-weight 23900 #checksum 9730

Query Match 16.8%; Score 263; DB 14; Length 214;
Best Local Similarity 25.4%; Pred. No. 1.49e-22;
Matches 33; Conservative 38; Mismatches 57; Indels 2; Gaps 2;

Db 61 dspavngatghs-ssldarevipmaavkqalreagdefelrlyrrafsdltsqhlhpgta 119
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 48 EAEgVAAPADPEMVTLPQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMLOHLQPTAENA 107
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 ygsfeqvnnelfrdgvnwgrivaffsgalcvsvdkemqvlsvraswmatylnhdh-1 178
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 108 YEFTKIATSLFESGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHC1 167
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 epwiqenggw 188
||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 168 ARWIAQRGGW 177

RESULT 8
ENTRY #type complete
TITLE transforming protein (bcl-2-beta) - chicken

```



```

QY 54 APADPEMTLP-LQPSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHQLPTAENAYEFT 112
Db 133 tvveelfrdgwnvgrivaffefggvmcvesvnrmsplvndialwteylnrh-lhtwiq 191
QY 113 KIATSLFESGINMGVRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIA 172
Db 192 dnggwqva 199
QY 173 QRGWVAA 180

RESULT 12
ENTRY TVHUAL #type complete
TITLE transforming protein bcl-2, splice form alpha - human
ORGANISM formal_name Homo sapiens #common_name man
DATE 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS A37332; A29409; S02452; A24428; A27622; B27622
REFERENCE A37332
#authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.
#accession C37332
##status nucleic acid sequence not shown; not compared with conceptual translation
##molecule_type DNA
##residues 1-239 ##label EGU
#note this report is a correction
REFERENCE A29409
#authors Tsujimoto, Y.; Croce, C.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
#accession A29409
##molecule_type mRNA
##residues 1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
#note this sequence has been corrected in reference A37332
REFERENCE S02452
#authors Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.B.; Goldman, P.; Korsmeyer, S.J.
#journal EMBO J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--Ig fusion gene in lymphoma.
#cross-references MUID:88196071
#accession S02452
##molecule_type mRNA
##residues 1-239 ##label SET
REFERENCE A24428
#authors Cleary, M.L.; Smith, S.D.; Sklar, J.
#journal Cell (1986) 47:19-28
#title Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t (14;18) translocation.
#cross-references MUID:87002488
#accession A24428
##molecule_type mRNA
##residues 1-58,'T',60-116,'R',118-239 ##label CLE
REFERENCE A27622
#authors Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
#journal Oncogene Res. (1988) 2:263-275
#title Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
#cross-references MUID:88217344
#accession A27622
##molecule_type mRNA
##residues 1-58,'T',60-239 ##label HUA
#accession B27622
##molecule_type DNA

```

```

##residues 1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2
#note the sequence was determined from the germline gene
COMMENT Constitutive expression of BCL2 following t(14;18) chromosomal translocation is typically found in follicular lymphoma.
GENETICS
#gene GDB:BCL2
##cross-references GDB:119031
#map_position 18q21.33-18q21.33
FUNCTION blocks apoptosis in hematopoietic cells
#description #superfamily bcl transforming protein
CLASSIFICATION alternative splicing; B-cell lymphoma; follicular lymphoma;
KEYWORDS proto-oncogene; transforming protein
SUMMARY #length 239 #molecular-weight 26266 #checksum 8323

Query Match 16.3%; Score 255; DB 2; Length 239;
Best Local Similarity 29.3%; Pred. No. 2.43e-21;
Matches 41; Conservative 37; Mismatches 57; Indels 5; Gaps 4;

Db 74 tpaapgaagpalspvpvvhlt--lrqagddfsrryrdfaemssqlhltptargra 131
QY 54 APADPEMTLP-LQPSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHQLPTAENAYEFT 112
Db 132 tvveelfrdgwnvgrivaffefggvmcvesvnrmsplvndialwteylnrh-lhtwiq 190
QY 113 KIATSLFESGINMGVRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIA 172
Db 191 dnggwqafvel-ygpsmrpl 209
QY 173 QRGWVAAALNLGNGPILNL 192

RESULT 13
ENTRY I67431 #type complete
TITLE BCL-x-Long - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I67431
REFERENCE I53295
#authors Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
#cross-references MUID:95129487
#accession I67431
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-233 ##label RES
#cross-references EMBL:U34963; NID:G1004376; CDS_PID:G1004377
SUMMARY #length 233 #molecular-weight 26122 #checksum 8310

Query Match 16.1%; Score 252; DB 14; Length 233;
Best Local Similarity 28.4%; Pred. No. 6.88e-21;
Matches 33; Conservative 31; Mismatches 50; Indels 2; Gaps 2;

Db 83 maavkqalreagdeflryrrafsdltslhltptgtyqsfvvnelfrdgwnvgriva 142
QY 71 MGQVGRQLAIGDDINRRYDSEFQTMQLHQLPTAENAYEFTKATSLFESGINMGVRVA 130
Db 143 sssfggacvsvdkengqvivsrvaswmatylnhdh-lepwqenggwtdtfdvlygn 197
QY 131 LLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGGWVAALNL-GN 185

RESULT 14
ENTRY TVMSB1 #type complete
TITLE transforming protein bcl-2-beta - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change

```

```

ACCESSIONS      02-Jun-1994
REFERENCE       B25960
#authors        Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
#journal        C.M.
#journal        Cell (1987) 49:455-463
#title          Molecular analysis of mbcl-2: structure and expression of the
#               murine gene homologous to the human gene involved in
#               follicular lymphoma.
#cross-references MUID:87187643
#accession      B25960
#molecule_type DNA
#residues       1-199 ##label NEG
GENETICS
#gene           BCL2
CLASSIFICATION  #superfamily bcl transforming protein
KEYWORDS        alternative splicing; transforming protein
SUMMARY         #length 199 #molecular-weight 22299 #checksum 7397

Query Match      16.0%; Score 250; DB 2; Length 199;
Best Local Similarity 31.1%; Pred. No. 1.38e-20;
Matches 32; Conservative 29; Mismatches 41; Indels 1; Gaps 1;

Db 94 lrragddfsrryrrdfaesqhlhptfgrgrfatvveelfrdgwnwgrivafefggv 153
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 78 LAIIGDDINRRYDSEFQTLQHQTAENAYEYFTKIATSLFESGINWGRVALLGFGYR 137
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 154 mcvesvrensplydnialwmtelylnrh-lhtwiqdnngwvga 195
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 138 LALHYQHGLTGLGQVTRFVDFMLHHCIAARQAGWVA 180

RESULT 15
ENTRY      TVNSAL      #type complete
TITLE      transforming protein bcl-2-alpha - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
           02-Jun-1994
ACCESSIONS A25960
REFERENCE   A90893
#authors    Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
#journal    C.M.
#journal    Cell (1987) 49:455-463
#title      Molecular analysis of mbcl-2: structure and expression of the
#           murine gene homologous to the human gene involved in
#           follicular lymphoma.
#cross-references MUID:87187643
#accession      A25960
#molecule_type DNA
#residues       1-236 ##label NEG
GENETICS
#gene        BCL2
#introns     192/3
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS      alternative splicing; transforming protein
SUMMARY       #length 236 #molecular-weight 26524 #checksum 6709

Query Match      16.0%; Score 250; DB 2; Length 236;
Best Local Similarity 30.4%; Pred. No. 1.38e-20;
Matches 35; Conservative 31; Mismatches 47; Indels 2; Gaps 2;

Db 94 lrragddfsrryrrdfaesqhlhptfgrgrfatvveelfrdgwnwgrivafefggv 153
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 78 LAIIGDDINRRYDSEFQTLQHQTAENAYEYFTKIATSLFESGINWGRVALLGFGYR 137
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 154 mcvesvrensplydnialwmtelylnrh-lhtwiqdnngwvga 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 138 LALHYQHGLTGLGQVTRFVDFMLHHCIAARQAGWVA 192

```

MPSRLH
***** (TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Aug 20 11:01:54 1997; MasPar time 6.20 Seconds
Tabular output not generated. 722.269 Million cell updates/sec

Title: >US-08-320-157-7
Description: (1-211) from US08320157.pgp
Perfect Score: 1561
Sequence: 1 MASGGGPPPRQECGEALP.....LVVLGVLLGQVVRFFKS 211
Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 47.042; Variance 90.697; scale 0.519

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description Pred. No.
1	274	17.6	1 BCLX_CHICK APOPTOSIS REGULATOR B 3.45e-30
2	270	17.3	233 1 BCLX_RAT APOPTOSIS REGULATOR B 1.95e-29
3	266	17.0	233 1 BCLX_HUMAN APOPTOSIS REGULATOR B 1.10e-28
4	261	16.7	233 1 BCL2_CHICK APOPTOSIS REGULATOR B 9.46e-28
5	255	16.3	205 1 BC2B_HUMAN PROTEIN BCL-2-BETA. 1.24e-26
6	255	16.3	239 1 BC2A_HUMAN PROTEIN BCL-2-BETA. 1.05e-25
7	250	16.0	199 1 BCL2_MOUSE PROTEIN BCL-2-BETA. 1.05e-25
8	250	16.0	236 1 BCL2_MOUSE PROTEIN BCL-2 ALPHA. 2.45e-25
9	248	15.9	236 1 BCL2_RAT PROTEIN BCL-2 ALPHA. 2.45e-25
10	218	14.0	192 1 BAXA_MOUSE APOPTOSIS REGULATOR B 7.08e-20
11	206	13.2	192 1 BAXA_HUMAN APOPTOSIS REGULATOR B 9.65e-18
12	201	12.9	218 1 BAXB_HUMAN APOPTOSIS REGULATOR B 7.31e-17
13	192	12.3	350 6 MCL1_HUMAN INDUCED MYELOID LEUKA 2.70e-15
14	177	11.3	143 1 BAXD_HUMAN BAX PROTEIN, CYTOPLAS 9.88e-13
15	176	11.3	172 5 HSAI_MOUSE HEMOPOIETIC-SPECIFIC 1.46e-12
16	140	9.0	179 3 EAR_ASFE4 APOPTOSIS REGULATOR B 9.67e-07
17	137	8.8	179 3 EAR_ASFE7 APOPTOSIS REGULATOR B 2.79e-06
18	134	8.6	179 3 EAR_ASFM2 APOPTOSIS REGULATOR B 7.95e-06
19	114	7.3	626 5 HTPG_BACSU HEAT SHOCK PROTEIN HT 6.32e-03
20	112	7.2	255 2 COX3_CAEEL CYTOCHROME C OXIDASE 1.19e-02
21	107	6.9	470 9 THRC_PSEAE THREONINE SYNTHASE (E 5.64e-02
22	106	6.8	133 4 GOP_BPP4 GOP PROTEIN. 7.65e-02

ALIGNMENTS									
RESULT	ID	BCLX_CHICK	STANDARD;	PRT;	190 AA.				
AC	Q07816;								
DT	01-FEB-1995	(REL. 31, CREATED)							
DT	01-FEB-1995	(REL. 31, LAST SEQUENCE UPDATE)							
DT	01-FEB-1995	(REL. 31, LAST ANNOTATION UPDATE)							
DE	APOPTOSIS REGULATOR BCL-X.								
GN	BCL-X.								
OS	GALLUS GALLUS (CHICKEN).								
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;								
OC	GALLIFORMES.								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE: 93364977.								
RA	BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L., LINDSTEN T.,								
RA	TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;								
RL	CELL 74:597-608(1993).								
CC	-!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.								
CC	-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH								
CC	LYMPHOID DEVELOPMENT.								
CC	-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.								
DR	EMBL; Z23110; G510899; -.								
DR	PIR; A47537; A47537.								
DR	PROSITE; PS01080; BCL2.								
KW	APOPTOSIS.								
SQ	SEQUENCE. 190 AA; 21467 MW; 7874E430 CRC32;								
Query Match 17.6%; Score 274; DB 1; Length 190;									
Best Local Similarity 28.2%; Pred. No. 3.45e-30;									
Matches 37; Conservative 33; Mismatches 59; Indels 2; Gaps 2;									
Db	60	vvgatvhrsslehvivasdvraqldagdefelrvrafsdltsqlhltptayqsf	119						
QY	52	VAAPADPEMVTLPQLQPSSTMGVGRQLAIIGDDINRRYDSEFQTMQLQHPATENAYEF	111						
Db	120	eqvvnelfhdgvnwgrivaffsfggalcvdesvdkmrvlgvgrivswmtctyltdh-ldpwi	178						
QY	112	TKTATSEFSGINWGRVALLGFGYRLALHYVGHGTGFLGQVTRFVDFMLHHCIARWI	171						
Db	179	qenggwvrtal 189							
QY	172	AQRGGNV-RAL 181							
RESULT	ID	BCLX_RAT	STANDARD;	PRT;	233 AA.				

P53563;
 01-OCT-1996 (REL. 34, CREATED)
 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCLX.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA MICHAELDIS T.M.;
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND
 CC BCL-X(S), ARE DERIVED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 DR EMBL; X82537; G607177; -.
 DR EMBL; X82537; G607178; -.
 KW APOPTOSIS; ALTERNATIVE SPLICING.
 FT VARSPLIC 126 188 MISSING (IN BCL-X(S)).
 SQ SEQUENCE 233 AA; 26130 MW; E0589815 CRC32;
 Query Match 17.3%; Score 270; DB 1; Length 233;
 Best Local Similarity 25.5%; Pred. No. 1.95e-29;
 Matches 36; Conservative 42; Mismatches 60; Indels 3; Gaps 3;
 Db 61 dspavngatghs-ssldarevlpmaavkqlreagdfefelrrafsdltsglhitppta 119
 QY 48 EAEQVAAPADPEMVTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLQPTAENA 107
 Db 120 yqsfegvnnelfdgvnwgrivaffsggalcvesvdkemqvlsvrtaammatylnhdh-1 178
 QY 108 YEFTKIATSLFESGINWGRVALLGFGYRLALHYQHGLTGLFGQVTRFVDFMLHCCI 167
 Db 179 epwiqnggwtdtfdlygna 199
 QY 168 ARWIAQRGGWVAALNL-GNGP 187
 RESULT 3
 ID BCLX_HUMAN STANDARD; PRT; 233 AA.
 AC Q07817;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCLX.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 93364977.
 RA BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
 RA LINDSTEN T., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;
 RL CELL 74:597-608(1993).
 CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND
 CC BCL-X(S), ARE DERIVED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 DR EMBL; Z23116; G629237; -.
 DR EMBL; Z23115; G510901; -.
 DR MTM; 600039; -.
 DR PROSITE; PS01080; BCL2.
 KW APOPTOSIS; ALTERNATIVE SPLICING.
 FT VARSPLIC 126 188 MISSING (IN BCL-X(S)).
 FT CONFLICT 70 70 G -> A (IN G510901).

SQ SEQUENCE 233 AA; 26049 MW; 57C67491 CRC32;
 Query Match 17.0%; Score 266; DB 1; Length 233;
 Best Local Similarity 25.5%; Pred. No. 1.10e-28;
 Matches 36; Conservative 42; Mismatches 60; Indels 3; Gaps 3;
 Db 61 dspavngatghs-ssldarevlpmaavkqlreagdfefelrrafsdltsglhitppta 119
 QY 48 EAEQVAAPADPEMVTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLQPTAENA 107
 Db 120 yqsfegvnnelfdgvnwgrivaffsggalcvesvdkemqvlsvrtaammatylnhdh-1 178
 QY 108 YEFTKIATSLFESGINWGRVALLGFGYRLALHYQHGLTGLFGQVTRFVDFMLHCCI 167
 Db 179 epwiqnggwtdtfdlygna 199
 QY 168 ARWIAQRGGWVAALNL-GNGP 187
 RESULT 4
 ID BCL2_CHICK STANDARD; PRT; 233 AA.
 AC Q00709;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE APOPTOSIS REGULATOR BCL-2.
 GN BCL-2.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92375724.
 RA EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
 RL NUCLEIC ACIDS RES. 20:4187-4192(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92379084.
 RA CAZALS-HATEM D.L., LOUIE D.C., TANAKA S., REED J.C.;
 RL BIOCHIM. BIOPHYS. ACTA 1132:109-113(1992).
 CC -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
 CC ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
 CC VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
 CC FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
 CC OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE
 CC (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 DR EMBL; D11382; G222794; -.
 DR EMBL; D11381; G222794; JOINED.
 DR EMBL; Z11961; G62970; -.
 DR PIR; A37332; A37332.
 DR PIR; S24390; S24390.
 DR PROSITE; PS01080; BCL2.
 KW APOPTOSIS; TRANSMEMBRANE; MITOCHONDRION.
 FT TRANSMEM 208 228 POTENTIAL.
 FT CONFLICT 64 64 G -> S (IN REF. 2).
 FT CONFLICT 67 82 G -> V (IN REF. 2).
 FT CONFLICT 121 121 H -> T (IN REF. 2).
 FT CONFLICT 139 139 G -> V (IN REF. 2).
 SQ SEQUENCE 233 AA; 25687 MW; 3376502C CRC32;
 Query Match 16.7%; Score 261; DB 1; Length 233;
 Best Local Similarity 28.5%; Pred. No. 9.46e-28;
 Matches 41; Conservative 41; Mismatches 57; Indels 5; Gaps 5;
 Db 60 hhrpeppgsaaasevppae-glrrapp-g-vhlalrqagdeferryrqdfagmgqlhlt 116
 QY 44 QQEQAEQVAAPADPEMVTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLQPT 103
 Db 117 pftahgrfvavveelfrdgvnwgrivaffegvgmvesvnmremslpvdnlatmteyln 176

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QY 104 AENAYEFTKIATSLFESGINWGRVALLGFGYRLALHVYOHGLTGLGQVTRFVDFML 163
Db 177 rh-lhnwqdgngwdafevlygns 199
QY 164 HHCIARWIAQRGGWVAALNL-GNG 186

RESULT 5
ID BC2B_HUMAN STANDARD; PRT; 205 AA.
AC P10416;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PROTEIN BCL-2-BETA.
GN BCL2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86259760.
RA TSUJIMOTO Y., CROCE C.M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96 AND 110.
RX MEDLINE; 92375724.
RA EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
RL NUCLEIC ACIDS RES. 20:4187-4192(1992).
RN [3]
RP SUBCELLULAR LOCATION.
RX MEDLINE; 91066924.
RA HOCKENBERRY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
RL NATURE 348:334-336(1990).
CC -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
CC FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
CC OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC -1- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
CC II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
CC T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
CC REGIONS.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC DIFFER AT THEIR C-TERMINAL ENDS.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; M13995; G179369; ALT_SEQ.
DR PIR; B29409; TVHUB1.
DR PIR; D37332; D37332.
DR MIM; 151430; -.
DR PROSITE; PS01080; BCL2.
KW PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE;
KW MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
SQ SEQUENCE 205 AA; 22311 MW; ED321E5E CRC32;

Query Match 16.3%; Score 255; DB 1; Length 205;
Best Local Similarity 29.7%; Pred. No. 1.24e-26;
Matches 38; Conservative 35; Mismatches 51; Indels 4; Gaps 3;

Db 74 tpaapgaagpalsvpvppvhl--lrqagddfsrryrrdfaemssqhlhltftargfa 131
QY 54 APADPEMTLP-LQPSSTMVGQVQLAIGDDINRRYDSEFTMLQLHLOPTAENAYEFT 112
Db 132 tvveelfrdgnwgrivaffegvgmvesvnrnsmplvldnialwmtelynrh-lhtwiq 190
QY 113 KIATSLFESGINWGRVALLGFGYRLALHVYOHGLTGLGQVTRFVDFMLHHCIAWIA 172
Db 191 dnggwaga 198
QY 173 ORGGWAA 180

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RESULT
ID BC2A_HUMAN STANDARD; PRT; 239 AA.
AC P10415;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PROTEIN BCL-2-ALPHA.
GN BCL2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86259760.
RA TSUJIMOTO Y., CROCE C.M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE; 92375724.
RA EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
RL NUCLEIC ACIDS RES. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87002488.
RA CLEARY M.L., SMITH S.D., SKLAR J.;
RL CELL 47:19-28(1986).
RN [4]
RP SUBCELLULAR LOCATION.
RX MEDLINE; 91066924.
RA HOCKENBERRY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
RL NATURE 348:334-336(1990).
CC -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
CC FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
CC OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC -1- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
CC II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
CC T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
CC REGIONS.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC DIFFER AT THEIR C-TERMINAL ENDS.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; M13994; G179367; ALT_SEQ.
DR PIR; M14745; G179371; -.
DR PIR; A29409; TVHUB1.
DR PIR; A24428; TVHUBC.
DR PIR; C37332; C37332.
DR MIM; 151430; -.
DR PROSITE; PS01080; BCL2.
KW PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE;
KW MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
FT TRANSMEM 212 233 POTENTIAL.
FT CONFLICT 59 59 P->T (IN REF. 3).
FT CONFLICT 117 117 S->R (IN REF. 3).
SQ SEQUENCE 239 AA; 26266 MW; 75084B59 CRC32;

Query Match 16.3%; Score 255; DB 1; Length 239;
Best Local Similarity 29.3%; Pred. No. 1.24e-26;
Matches 41; Conservative 37; Mismatches 57; Indels 5; Gaps 4;

Db 74 tpaapgaagpalsvpvppvhl--lrqagddfsrryrrdfaemssqhlhltftargfa 131
QY 54 APADPEMTLP-LQPSSTMVGQVQLAIGDDINRRYDSEFTMLQLHLOPTAENAYEFT 112
Db 132 tvveelfrdgnwgrivaffegvgmvesvnrnsmplvldnialwmtelynrh-lhtwiq 190
QY 113 KIATSLFESGINWGRVALLGFGYRLALHVYOHGLTGLGQVTRFVDFMLHHCIAWIA 172

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QY 47 QAEAGVAAPADPENVTLPQSSMTGQVGR-QLAIGDDINRRYDSEFQMLQHQLTAE 105
Db 122 tagrftatveelfrdvngvriavfaffegvmcgvsnremslvndialwmtelylnrh 181
QY 106 NAYEYFTKIATSLFESGINSRVVALLGFGYRLALHYQHGLTGLGQVTRFVVDMLH 165
Db 182 -lhtwqdgngwafvel-ygppmrpl 206
QY 166 CIARWIAQRGGVAAALNLGNGPILNLV 192

RESULT 10
ID BAXA_MOUSE STANDARD; PRT; 192 AA.
AC Q07813;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DE APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN BAX.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X DBA/2 F1;
RX MEDLINE; 93364978.
RA OLTVAI Z.N., MILLMAN C.L., KORSMEYER S.J.;
RL CELL 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L22472; G388192; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21394 MW; BD035304 CRC32;

Query Match 14.0%; Score 218; DB 1; Length 192;
Best Local Similarity 25.6%; Pred. No. 7.08e-20;
Matches 46; Conservative 50; Mismatches 75; Indels 9; Gaps 8;

Db 16 seqlmktgafllqfigdragmagetpeltleqpddastk-klseclrriqdelds-- 72
QY 31 TEEVFRSYVYRHOQEAEGVAAPADPEM-VTLPLQPSSTMGVGRQLAIGDDINRRY 89
Db 73 nmelqrlmadvtdtspre-vff-tvaadmfadgnfnvgrvvalfyfaskivlkalctkvp 130
QY 90 DSEFQMLQHQLTAE NAYEYFTKIATSLFESG-INNGRVVALLGFGYRLALHYQHGLT 148
Db 131 elittingwtldf-lrerllwldqggwgllyfqtptwtvtifvagvltasltiwlk 189
QY 149 GFLGQVTRFVVDMLHHCIARWIAQRGGVAAALNLGNGPI-LNLVLVGVLLGQFVVR 207

RESULT 11
ID BAXA_HUMAN STANDARD; PRT; 192 AA.
AC Q07812;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DE APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN BAX.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=B-CELL;
RX MEDLINE; 93364978.
RA OLTVAI Z.N., MILLMAN C.L., KORSMEYER S.J.;
RL CELL 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L22473; G388166; -.
DR PIR; A47538; A47538.
DR MIM; 600040; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21184 MW; B2E61484 CRC32;

Query Match 13.2%; Score 206; DB 1; Length 192;
Best Local Similarity 24.5%; Pred. No. 9.65e-18;
Matches 40; Conservative 45; Mismatches 71; Indels 7; Gaps 6;

Db 32 qdragrmggeapelaldpvpqdastklseclkrigdeldd--nmelqrlmadvtdtspr 89
QY 47 QAEAGVAAPADPEMVTLPQPSSTMGVGRQLAIGDDINRRYDSEFQMLQHQLTAE 106
Db 90 e-vff-rvaadmfadgnfnvgrvvalfyfaskivlkalctkvpelittingwtldf-lre 146
QY 107 AYEYFTKIATSLFESG-INNGRVVALLGFGYRLALHYQHGLTGLGQVTRFVVDMLH 165
Db 147 rllgwldqggwgllyfqtptwtvtifvagvltasltiwlk 189
QY 166 CIARWIAQRGGVAAALNLGNGPI-LNLVLVGVLLGQFVVR 207

RESULT 12
ID BAXB_HUMAN STANDARD; PRT; 218 AA.
AC Q07814;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE APOPTOSIS REGULATOR BAX, CYTOPLASMIC ISOFORM BETA.
GN BAX.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RX MEDLINE; 93364978.
RA OLTVAI Z.N., MILLMAN C.L., KORSMEYER S.J.;
RL CELL 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L22474; G388168; -.
DR PIR; B47538; B47538.
DR MIM; 600040; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS; ALTERNATIVE SPLICING.
SQ SEQUENCE 218 AA; 24220 MW; 82B2FF09 CRC32;

Query Match 12.9%; Score 201; DB 1; Length 218;
Best Local Similarity 27.0%; Pred. No. 7.31e-17;
Matches 37; Conservative 36; Mismatches 58; Indels 6; Gaps 5;

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Db 32 qdrgnngsepelaldpvpdgaatklklseclkrigdelde--mmelqrmaavtdsdr 89
Qy 47 OEAEGVAAPADPENVTLPLQSPSSMGVGRQLAIIGDDINRRYDSEFQTMQLHQPATAEN 106
Db 90 e-vff-zvaedmfadgnfngrvvalfyfasklvtkalctkvpelirtngwtldf-lre 146
Qy 107 AYEFTKIATSLFESG-INMGVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDFMLH 165
Db 147 rllgwigdgggwwllk 163
Qy 166 CIARWIAQGGGWAALN 182

RESULT 13
ID MCL1_HUMAN STANDARD; PRT; 350 AA.
AC Q07820;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1.
GN MCL1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MYELOID LEUKEMIA CELLS;
RX MEDLINE; 93234528.
RA KOZOPAS K.M., YANG T., BUCHAN H.L., ZHOU P., CRAIG R.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:3516-3520(1993).
CC -1- FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTIATION AND
CC CONCOMITANT MAINTENANCE OF VIABILITY BUT NOT OF PROLIFERATION
CC (PROBABLE).
CC -1- INDUCTION: EXPRESSION INCREASES EARLY DURING PHORBOL-ESTER INDUCED
CC DIFFERENTIATION ALONG THE MONOCYTE/MACROPHAGE PATHWAY IN MYELOID
CC LEUKEMIA CELL LINES ML-1.
CC -1- SIMILARITY: BELONGS TO THE BCL2 FAMILY.
DR EMBL; L08246; -; NOT_ANNOTATED_CDS.
DR PIR; A47476; A47476.
DR MIM; 159552; -
DR PROSITE; PS01080; BCL2
KW APOPTOSIS; TRANSMEMBRANE; DIFFERENTIATION.
FT UNSURE 227 OR A.
FT TRANSMEM 330 349 POTENTIAL.
SQ SEQUENCE 350 AA; 37365 MW; 10194864 CRC32;

Query Match 12.3%; Score 192; DB 6; Length 350;
Best Local Similarity 24.3%; Pred. No. 2.70e-15;
Matches 34; Conservative 40; Mismatches 63; Indels 3; Gaps 3;

Db 174 lyrgselelsrlyreqatgkdktpmrgsatsrkaletlrrvgdvgrnhetvfgqmlr 233
Qy 40 FYRHQQGEAGVAAPADPENVTLPLQSPSSMGVGRQ-LAIIGDDINRRYDSEFQTMQLQ 98
Db 234 kldlkneddvkslrvmlhvfsgdvtnwgrvrltvlslsfafvkhkltngesclepleas 293
Qy 99 HLOPTAENAYEYFTKIATSLFESGI-NMGVVALLGFGYRLALHYVQHGLTGFLGQVTRF 157
Db 294 itd-vlvrtkrdwlvkqrgw 312
Qy 158 VVDFMLHHCIARWIAQGGW 177

RESULT 14
ID BAXD_HUMAN STANDARD; PRT; 143 AA.
AC PS5269;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE BAX PROTEIN, CYTOPLASMIC ISOFORM DELTA.
GN BAX.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95331797.
RA APTE S.S., MATTEI M.-G., OLSEN B.R.;
RL GENOMICS 26:592-594(1995).
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; U19599; G841238; -
DR MIM; 600040; -
KW APOPTOSIS; ALTERNATIVE SPLICING.
SQ SEQUENCE 143 AA; 15772 MW; 71AA1CBD CRC32;

Query Match 11.3%; Score 177; DB 1; Length 143;
Best Local Similarity 27.4%; Pred. No. 9.88e-13;
Matches 29; Conservative 31; Mismatches 43; Indels 3; Gaps 3;

Db 36 tdsprevfrrvaadmfadgnfngrvvalfyfasklvtkalctkvpelirtngwtldf- 94
Qy 104 AENAYEFTKIATSLFESG-INMGVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDFM 162
Db 95 lrerllgwigdgggllsyfgtwtvtvtfvavgtasltiwlk 140
Qy 163 LHHCIARWIAQGGGWAALNMGNGPI-LNVLVGVLLGQFVVR 207

RESULT 15
ID HSAL_MOUSE STANDARD; PRT; 172 AA.
AC Q07440;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN (A1 PROTEIN).
GN A1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/J; TISSUE=BONE MARROW;
RX MEDLINE; 93346743.
RA LIN E.Y., ORLOFSKY A., BERGER M.S., PRYSTOWSKY M.B.;
RL J. IMMUNOL. 151:1979-1988(1993).
CC -1- FUNCTION: MAY FUNCTION IN THE RESPONSE OF HEMOPOIETIC CELLS TO
CC EXTERNAL SIGNALS.
CC -1- INDUCTION: BY GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR
CC AND LPS IN MACROPHAGES.
CC -1- SUBCELLULAR LOCATION: INTRACELLULAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEMOPOIETIC TISSUES, INCLUDING
CC BONE MARROW, SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L16462; G293274; -
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS.
FT DOMAIN 24 33 ALA/PRO-RICH.
SQ SEQUENCE 172 AA; 19914 MW; FFD38D6F CRC32;

Query Match 11.3%; Score 176; DB 5; Length 172;
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Matches 33; Conservative 29; Mismatches 46; Indels 6; Gaps 6;

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Db 88 rvtifafgvlkkllpqeqialdvcaykqvsstfaevfmmn-tgwlirnggw 140
Qy 127 RVVALLGFG-YRLA-LHYVQHGLTG-FLGQVTRFVVDFMLHHCIARWIAQGGW 177

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Search completed: Wed Aug 20 11:02:15 1997
Job time : 21 secs.



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W P S R L H
(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.
MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Aug 21 12:30:31 1997; MasPar time 1065.82 Seconds
Tabular output not generated.
Title: >US-08-320-157-8
Description: (1-1287) from US08320157.seq
Perfect Score: 1287
N.A. Sequence: 1 TTTTAATATAAATTAATGTG.....CCTCAAGAGTACAGAAGCTT 1287
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Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 362067 seqs, 549138275 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: emb1-new3
1: BCT 2: FUN 3: GEN1 4: GEN2 5: HTG1 6: HTG2 7: HUM 8: INV
9: ORG 10: MAM 11: VRT 12: PLN 13: PRO 14: ROD 15: SYN 16: UNC
17: VRL
Database: genbank99
18: BCT1 19: BCT2 20: BCT3 21: BCT4 22: BCT5 23: BCT6 24: BCT7
25: BCT8 26: BCT9 27: BCT10 28: BCT11 29: GEN1 30: GEN2
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38: INV4 39: INV5 40: INV6 41: INV7 42: INV8 43: INV9 44: INV10
45: INV11 46: MAM1 47: MAM2 48: MAM3 49: VRT1 50: VRT2 51: VRT3
52: VRT4 53: PAT1 54: PAT2 55: PAT3 56: PAT4 57: PAT5 58: PHG
59: PLN1 60: PLN2 61: PLN3 62: PLN4 63: PLN5 64: PLN6 65: PLN7
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85: ROD1 86: ROD2 87: ROD3 88: ROD4 89: ROD6 90: ROD6 91: ROD7
92: ROD8 93: STR 94: SYN 95: UNA 96: VRL1 97: VRL2 98: VRL3
99: VRL4 100: VRL5 101: VRL6 102: VRL7 103: VRL8 104: VRL9
105: VRL10
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112: MAM 113: VRT 114: PHG 115: PLN 116: PRI1 117: PRI2
118: ROD 119: SYN 120: UNA 121: VRL
Database: u-emb150_99
122: parti
Statistics: Mean 11.725; Variance 5.132; scale 2.285
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

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1	1269	98.6	6478	77	Human Bak-2 gene, com	0.00e+00
2	894	69.5	1360	73	H.sapiens BAK mRNA fo	0.00e+00
3	890	69.2	2094	77	Human Bak mRNA, compl	0.00e+00
4	768	59.7	1949	77	Human Bak protein mRN	0.00e+00
5	753	58.5	5408	77	Human Bak-3 pseudogen	0.00e+00
6	198	15.4	123579	5	Human DNA sequence **	3.97e-149
7	177	13.8	444	70	Human DNA for apoptosi	1.52e-129
8	88	6.8	140	70	Human DNA for apoptosi	4.96e-49
9	37	2.9	215	57	Sequence 5 from paten	4.92e-08
10	35	2.7	215	57	Sequence 5 from paten	1.16e-06
11	27	2.1	250	82	Homo sapiens platelet	1.44e-01
12	27	2.1	1049	45	T.thermophila G8-scrn	1.44e-01
13	27	2.1	2648	44	Plasmodium falciparum	1.44e-01
14	27	2.1	9747	52	X.laavis POMC-A gene	1.44e-01
15	26	2.0	610	45	Xenos pecki 28S ribos	5.48e-01
16	26	2.0	2006	22	Enterococcus faecalis	5.48e-01
17	26	2.0	2759	43	Leishmania tarentolae	5.48e-01
18	26	2.0	20992	42	Leishmania tarentolae	5.48e-01
19	26	2.0	91017	117	Human DNA sequence fr	5.48e-01
20	26	2.0	91017	7	Human DNA sequence fr	5.48e-01
21	26	2.0	91022	33	Human DNA sequence **	5.48e-01
22	26	2.0	129207	34	Human DNA sequence **	5.48e-01
23	24	1.9	1055	85	M.musculus gast gene	7.12e+00
24	24	1.9	1630	63	W.suaveolens mitochon	7.12e+00
25	25	1.9	1812	105	Vesicular stomatitis	2.01e+00
26	25	1.9	1812	105	Vesicular stomatitis	2.01e+00
27	24	1.9	1862	64	Pyromyces sp. mRNA fo	7.12e+00
28	24	1.9	2220	39	D.discoideum CABP1 ge	7.12e+00
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30	24	1.9	2857	74	Human transcripition f	7.12e+00
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32	24	1.9	4484	61	C.roseus strl gene.	7.12e+00
33	25	1.9	5745	20	C.perfringens DNA for	2.01e+00
34	24	1.9	7792	41	D.melanogaster fish me	7.12e+00
35	25	1.9	7849	67	Soybean phytochrome B	2.01e+00
36	24	1.9	17279	52	Snake (habu) gTfBP g	7.12e+00
37	25	1.9	17366	52	Snake (green habu) gT	2.01e+00
38	24	1.9	29203	37	Caenorhabditis elegans	7.12e+00
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42	24	1.9	37136	117	Human DNA sequence fr	7.12e+00
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45	24	1.9	110384	73	Human BAC clone RG062	7.12e+00

ALIGNMENTS

1 H5U16812 6478 bp DNA PRI 19-AUG-1995
LOCUS Human Bak-2 gene, complete cds.
DEFINITION H5U16812
ACCESSION U16812
NID g595925
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 6478)
AUTHORS Kiefer, M.C., Brauer, M.J., Powers, V.C., Wu, J.J., Umansky, S.R.,
Tomel, L.D. and Barr, P.J.
TITLE Modulation of apoptosis by the widely distributed Bcl-2 homologue
Bak
JOURNAL Nature 374 (6524), 736-739 (1995)
MEDLINE 95231654
REFERENCE 2 (bases 1 to 6478)
AUTHORS Kiefer, M.C.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) Michael C. Kiefer, Mol. Biol., LXR

Biotechnology Inc., 1401 Marina Way South, Richmond, CA 94804, USA
Location/Qualifiers
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FEATURES
source

CDS

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Qy 121 AGCCACGTCCATAGTTCTATTATTAGATTCTTCCCTTTATACAGATTATTATAGCTTC 180

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Qy 1259 AGGG-TCCCCCCTCAAGAGTACAGAAGCTT 1287

RESULT 2

LOCUS HSCBP1 1360 bp RNA PRI 05-MAY-1995
DEFINITION H.sapiens BAK mRNA for BCL-2 homologue.
ACCESSION X84213

NID g804984

KEYWORDS Bcl-2 protein; CEBP-1 gene.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1360)

AUTHORS Farrow,S.N., White,J.H., Martinou,I., Raven,T., Pun,K.T.,

Grinham,C.J., Martinou,J.C. and Brown,R.

Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K

Nature 374 (6524), 731-733 (1995)

MEDLINE 95231652

REMARK Erratum:[Nature 1995 Jun 1;375(6530):431]]

REFERENCE 2 (bases 1 to 1360)

AUTHORS Brown,R.

TITLE Direct Submission

Submitted (25-JAN-1995) R. Brown, Glaxo Research & Development,

Greenford Road, Greenford, Middlesex UB6 0HE, UK

JOURNAL Location/Qualifiers

FEATURES

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QY	592	CCTGCCCTGCCCTGTCTTCTGAGGAGCAGGTAGCCAGGACACAGAGGAGGTTTCCGC	651		
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QY	652	AGCTACGTTTTTTACCAACATCACAGAACAGGAGGCTGAAGGGGGCGCTGCCCTGCC	711		
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DEFINITION	Human Bak mRNA, complete cds.				
ACCESSION	U16811				
NID	9595923				
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 2094)				
REFERENCE	Kiefer, M.C., Brauer, M.J., Powers, V.C., Wu, J.J., Umansky, S.R., Tomei, L.D. and Barr, P.J.				
AUTHORS	Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak				
TITLE	Nature 374 (6524), 736-739 (1995)				
JOURNAL	95231654				
MEDLINE	2 (bases 1 to 2094)				
REFERENCE	Kiefer, M.C.				
AUTHORS	Direct Submission				
TITLE	Submitted (02-NOV-1994) Michael C. Kiefer, Mol. Biol., LXR Biotechnology Inc., 1401 Marina Way South, Richmond, CA 94804, USA				
JOURNAL	Location/Qualifiers				
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ORIGIN					
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Mismatches	917; Conservative 0; Mismatches 15; Indels 2; Gaps 2;				
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QY	355	GGGACAAGTAAAGGCTACATCCAGATCTGGGAATGCACTGACGCCATTCCTGGAACT	414		
Db	73	ggctcccaactcagccctggagcagcagccgacccctcgg-acctccattctcac	131		
QY	415	GGGTCCCACTCAGCCCTGGGAGCAGCAGCCGCCCTCGGGACCTCCATCTCCAC	474		
Db	132	cctgtgagccacccgggttgggccaagatcccgcgaggtgactccctctccactgag	191		
QY	475	CTGTCTGAGCCACCCGGTGGGCCAGGATCCCGCAGGCTGATCCCGTCTCTCCACTGAG	534		
Db	192	acctgaaaaatggcttcgggccaaggccccagggtctctccaggcaggaggtcgaggagcct	251		
QY	535	ACCTGAAAAATGGCTTCGGGGCAAGGCCAGGTCTCTCCAGGAGGAGTGGGAGAGCCT	594		
Db	252	gccctgacctctgtcttctgagggcaggttagccagagacacagagggttttccgcagc	311		
QY	595	GCCTGGCCCTCTGCTTCTGAGGACAGGTAGCCAGGACACAGAGGAGGTTTCCCGAGC	654		
Db	312	taqgtttttaccgccatcagcaggaacagaggtgctgaaggggtgctgccctgcccag	371		
QY	655	TAGCTTTTTTACCACCATCAGCAGGAACAGAGGCTGAAGGGCGGCTGCCCTGCCGAC	714		
Db	372	ccagagatggttcaccttacctcttcaaccttagcagaccattggggcagggtgggacggcag	431		

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QY 715 CCAGAGATGGTCACCTTACCTCTGCAACCTAGCAGCACCATGGCGAGGTGGGAGCGCAG 774
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QY 775 CTCGCCATCATTTGGGAGGACATCAACCGAGCGTATGACTCAGAGTTCAGAGACCATTTG 834
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QY 835 CAGCACCTGCAGCCAGCGGAGAGAACTGCTATGACTTACTTCCACCAAGATTGCCATCCAGC 894
Db 552 CTGTTGAGAGTGGATCAATATGGGCGCGTGTGTGCTCTTCTGGGCTTCAGCTACCGT 611
QY 895 CTGTTTGGAGAGTGGATCAATATGGGCGCGTGTGTGCTCTTCTGGGCTTCAGCTACCGT 954
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QY 955 CTGGCCCTACACATCTACACAGCTGGCTGACTGGCTTCTTGGGCCAGGTGACCCGCTT 1014
Db 672 GTGGTGCATCTCATGCTGCATCACTGATTCGCCGCTGATTCACCAAGATTGCCATCCAGC 731
QY 1015 GTGGTGCATCTCATGCTGCATCACTGATTCGCCGCTGATTCACCAAGATTGCCATCCAGC 1074
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QY 1075 GTGGCAGCCCTGAATTTGGGCAATGGTCCCATCTGAACTGCTGGTGTGCTGGTGTG 1194
Db 792 GTTCTGTGGGCGAGTTGTGGTACGAGATTTCTCAATCATGACTCCCAAGGGTGCCT 851
QY 1135 GTTCTGTGGGCGAGTTGTGGTACGAGATTTCTCAATCATGACTCCCAAGGGTGCCT 1194
Db 852 TTTGGTCCCGGTTTCAAGCCCTGCTGAGTTCAGGAGTTCAGGAGTTCAGGAGTTCAGGAG 911
QY 1195 TTTGGGTCCTGATTCAGACCCCTGCTGGAGTTCAGGAGTTCAGGAGTTCAGGAGTTCAGGAG 1254
Db 912 CTTGAGGTTCCCTCCCTCAAGAGTACAGAGCTT 945
QY 1255 -TTGAGGTTCCCTCCCTCAAGAGTACAGAGCTT 1287

RESULT 4
LOCUS HSU23765 1949 bp mRNA PRI 29-MAR-1996
DEFINITION Human Bak protein mRNA, complete cds.
ACCESSION U23765
NID 9758797
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1949)
AUTHORS Lutz R.J., Evan, G.I. and Guild, B.C.
Chittenden, T., Harrington, E.A., O'Connor, R., Flemington, C.,
Lutz, R.J., Evan, G.I. and Guild, B.C.
TITLE Induction of apoptosis by the Bcl-2 homologue Bak
JOURNAL Nature 374 (6524), 733-736 (1995)
MEDLINE 95231653
REFERENCE 2 (bases 1 to 1949)
AUTHORS Chittenden, T.
Direct Submission
TITLE Submitted (30-MAR-1995) Thomas Chittenden, Apoptosis Technology
JOURNAL Inc., 148 Sidney St., Cambridge, MA 02139, USA
FEATURES
source 1..1949
location/Qualifiers
CDS
1..1949
/organism="Homo sapiens"
/clone_lib="Jurkat cell cDNA library (Stratagene)"
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65..700
/function="induction of apoptosis"
/codon_start=1
/product="Bak protein"
/db_xref="PDB:1G58798"
/translation="MASGGQGGPPRQCGEPALPFSASEQVAQDTEVFRSYYVYRQ
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Matches 794; Conservative 0; Mismatches 14; Indels 2; Gaps 2;
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QY 480 TGAGCCACC CGGGTTGGGCCAGGATCCGCGAGGCTATCCGCTCCCTCCACTGAGACCTG 539
Db 61 aaaaatggtcttcgggcaagccaggctctcccaggcaggagtgcgagagacctgcct 120
QY 540 AAAAATGGCTTCGGGGGCAAGCCAGGCTCTCCAGGACAGAGTGGCGAGAGCTTGCCT 599
Db 121 gccctctgcttcgaggagcaggtagcccgaggacacagagaggttttccgcagctacgt 180
QY 600 GCCCTCTGCTTCTGAGGAGCAGGTAGCCAGGACACAGAGAGAGGTTTCCGCGACTAGCT 659
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QY 660 TTTTATACCATCATCAGCAGGAACAGGAGGCTGAAGGGCGGCTGCCCTGCCGACCCAGA 719
Db 241 gatggtcaccttacctctgcaacctagcaccatagcaccatggggcagggtggagagcgtcgc 300
QY 720 GATGGTCACCTTACCTCTGCAACCTAGCAGCACCATTGGGACAGTGGGACGGCAGCTGCG 779
Db 301 catcatcggggagcagacatacaccgacgctatgactcagagttccagaccatgttgcagca 360
QY 780 CATCATTTGGGAGCAGACATCAACCGACGCTATGACTCAGAGTTCAGAGACCATTTGCGAGCA 839
Db 361 cctgcagccacacggcagagagatgctatgacttacttccacaaagattgccacccacctgtt 420
QY 840 CCTGCAGCCACGCGCAGAGAAATGCTATGATGACTTACCAAGATTGCCCTCCAGCCCTGTT 899
Db 421 tgagagtgccatcaaatggggcggtggtggtctctctgggttcgggttcacctgcgc 480
QY 900 TGAGAGTGGGATCAATTTGGGGCGCGTGTGGTGGCTTCTTCTGGGCTTCAGCTACCGTCTGCG 959
Db 481 cctacacgtctaccagcatggcctgactggtctctcagcagcaggtgacccgcttcgtggt 540
QY 960 CTTACACATCTACCAGCGTGGCTGACTGGCTTCTTCTGGGCCAGGTTGACCGCTTTGGT 1019
Db 541 cgactcatcgtgcatacactgcatgcccgggtggattgcacagaggggtggtgggtggc 600
QY 1020 GGACTTTCATGCTGCATCAGTGCATTTGCCCGGTGGATTGCACAGAGGGGTGGCTGGGTGGC 1079
Db 601 agccctgaacttgggcaatggtcccatcctcagcagtgctggttctggtggtggttct 660
QY 1080 AGCCCTGAATTTGGGCAATGGTCCCATCTCCAGCTGCTGGTGGTCTGGGTGGTCT 1139
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QY 1140 GTTGGGCCAGTTTGTGTGTACGAAGATTCTCAATCATGACTCCCAAGGGGTGGCTTTGGG 1199
Db 721 gtcccgttcagacccccctgctggacttaagcgaagtctttgctctctctgttcccttgc 780
QY 1200 GTCCCACTTCAGACCCCTGCTGGAGTTAAGCGAAGCTTTTGGCTTCTCTGCTCC-TTGC 1258
Db 781 aggggtccccctcaagagtacagaagctt 810
QY 1259 AGGG-TCCCCCTTCAGAGGTACAGAGCTT 1287

RESULT 5
LOCUS HSU16813 5408 bp DNA PRI 19-AUG-1995
DEFINITION Human Bak-3 pseudogene, complete cds.
ACCESSION U16813
NID 9595927
KEYWORDS
SOURCE human.
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ID	HS291J10	standard; DNA; HTG; 133579 BP.	
AC	293017;		
NI	ei041698		
DT	19-MAR-1997 (Rel. 51, Created)		
DE	19-MAR-1997 (Rel. 51, Last updated, Version 1)		
DT	Human DNA sequence *** SEQUENCING IN PROGRESS ***	from clone 291J10	
KW	HTG; HTGS_PHASE1.		
OC	Homo sapiens (human)		
OS	Eukaryotae; mitochondrional eukaryotes; Metazoa; Chordata;		
NC	Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
RN	1-123579		
RP	Beck S.;		
RA			
RT			
RL	Submitted (06-NOV-1996) to the EMBL/GenBank/DBJ databases.		
RL	Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA,		
RL	UK. E-mail enquires: humquersanger.ac.uk Clone requests:		
RL	clonerequest@sanger.ac.uk		
CC	IMPORTANT: This sequence is unfinished and does not necessarily		
CC	represent the correct sequence. Work on the sequence is in progress		
CC	and		
CC	the release of this data is based on the understanding that the		
CC	sequence may change as work continues. The sequence may be		
CC	contaminated		
CC	with foreign sequence from E.coli, yeast, vector, phage etc.		
CC	Order of segments is not known; 800 n's separate segments.		
CC	Unfinished sequence: dj291j10 Contig_ID: 01371 Length: 3951 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01623 Length: 1040 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 00751 Length: 6361 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01422 Length: 1722 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 00105 Length: 26804 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01527 Length: 1598 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01231 Length: 1547 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01408 Length: 2194 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 00133 Length: 4250 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01390 Length: 4036 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01463 Length: 7484 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 00255 Length: 14415 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01327 Length: 9377 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 01441 Length: 6493 bp		
CC	Unfinished sequence: dj291j10 Contig_ID: 00931 Length: 21107 bp		
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FH			
FT	source	1..123579	
FT		organism="Homo sapiens"	

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FT      /chromosome="6"
SQ      Sequence 123579 BP; 28765 A; 27932 C; 27951 G; 27528 T; 11403 other;

Query Match      15.4%; Score 198; DB 5; Length 123579;
Best Local Similarity 98.6%; Pred. No. 3,97e-149;
Matches 206; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Db 107852 gctggcacctctatgacactggagctctcgcggtccctcggtgcacagggacagta 107911
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QY 306 GCTGGCACCTC-ATGATCACATGGAGTCTCGGGGTCCCTCAGGCTGCACAGGGACAAGTA 364
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Db 107912 aagctacatccagatgcgggaatgactgacgcccattctctggaactgggtccac 107971
|||||
QY 365 AAGGCTACATCCAGATGCTGGGAATGCACTGACGCCCATTCCTGGAAACTGGGTCCAC 424
|||||

Db 107972 tcagccctggagcagcagccgcccctcggtccctcggtccatctccacactcagc 108031
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QY 425 TCAGCCCTGGGACAGAGCGCCGCGCCCTCGGACCTCCATCTCCACCCTGCTGAGC 484
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Db 108032 caccgggttgggcaggatccccggcagg 108060
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QY 485 CACCCGGTTGGCCAGATCCCGCAGG 513
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RESULT 7
LOCUS      D88396S2      444 bp      DNA      PRI      10-JAN-1997
DEFINITION Human DNA for apoptosis-regulator Bak, exon 2, 3 and partial cds.
ACCESSION      D88397
NID      g1655492
KEYWORDS      Bak; apoptosis-regulator.
SEGMENT      2 of 2
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 444)
AUTHORS      Eguchi,H.
TITLE      Direct Submission
JOURNAL      Submitted (14-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hidetaka Eguchi, Saitama Cancer Center Research Institute,
Department of Biochemistry; 818 Komuro, Ina, Kita-adachi-gun,
Saitama 362, Japan (E-mail:hidesaitama-cc.go.jp,
Tel:048-722-1111(ex.255), Fax:048-722-1739)
REFERENCE      2 (bases 1 to 444)
AUTHORS      Eguchi,H. and Hayashi,S.
TITLE      Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL
and Bak, as well as susceptibility to therapeutic agents of human
breast cancer cells
JOURNAL      Unpublished (1996)
FEATURES      Location/Qualifiers
source      1..444
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              join(D88396:26..90,51..231,358..>444)
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ORIGIN
Query Match      13.8%; Score 177; DB 70; Length 444;

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Best Local Similarity 95.9%; Pred. No. 1.52e-129;
Matches 185; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 885 TGCCTCAGCCTGTTTGAGAGTGGCATCAATTTGGGGCCGTGTGTGGCTTCTTGGGCTT 944
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Db 102 cggtaacctctggccctacacgctctaccagcatggcctgactggcttccctagggcaggt 161
|||||
QY 945 CAGTACCGCTGTGGCCCTACACATCTACACAGCTGCGCTGACTGGCTTCTGGGCCAGGT 1004
|||||

Db 162 gaccgcttctggtgcactcatgctgcatcactgattgcccgtggtgattgcacagag 221
|||||
QY 1005 GACCCGCTTTGTGTGGACTTCATGTCATCTGTCATCTGCAATTCGCCGTGGATTGCACAG 1064
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Db 222 ggtggctgggtg 234
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QY 1065 GGTGGCTGGGTG 1077
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RESULT 8
LOCUS      D88396S1      140 bp      DNA      PRI      05-DEC-1996
DEFINITION Human DNA for apoptosis regulator Bak, exon 1.
ACCESSION      D88396
NID      g1655491
KEYWORDS      apoptosis-regulator; Bak.
SEGMENT      1 of 2
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 140)
AUTHORS      Eguchi,H.
TITLE      Direct Submission
JOURNAL      Submitted (14-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Hidetaka Eguchi, Saitama Cancer Center Research Institute,
Department of Biochemistry; 818 Komuro, Ina, Kita-adachi-gun,
Saitama 362, Japan (E-mail:hidesaitama-cc.go.jp,
Tel:048-722-1111(ex.255), Fax:048-722-1739)
REFERENCE      2 (bases 1 to 140)
AUTHORS      Eguchi,H. and Hayashi,S.
TITLE      Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL
and Bak, as well as susceptibility to therapeutic agents of human
breast cancer cells
JOURNAL      Unpublished (1996)
FEATURES      Location/Qualifiers
source      1..140
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              /clone="pGEMBak01-02"
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              /number=1
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BASE COUNT      33 a 52 c 27 g 28 t
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Query Match      6.8%; Score 88; DB 70; Length 140;
Best Local Similarity 98.9%; Pred. No. 4.96e-49;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 acgtatgactcagagtccagaccatgttgcagcactgctgaccccgccagcagaatgc 60
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QY 804 ACGTATGACTCAGAGTTCAGACCATTGTGCAGCACCTGCAGCCCGCAGGAGAAATGC 863
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Db 61 ctatgagtacttccaccaagattgccaccag 90
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QY 864 CTATGAGTACTTCCACCAAGATTGCTCCAG 893
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RESULT 9
LOCUS      128278      215 bp      DNA      PAT      30-OCT-1996
DEFINITION Sequence 5 from patent US 5569830.
ACCESSION      128278

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[illegible]

Nucleic Acids Res. 20 (4), 912 (1992)
 MEDLINE 92178994
 COMMENT See also M14555.
 FEATURES
 source Location/Qualifiers
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 299..325 /note="heat shock elements (2)"
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 QY 85 AAGATGAAAGTAAAAACAA 104
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 RESULT 13
 LOCUS PFTUBAI 2648 bp DNA INV 25-MAR-1993
 DEFINITION Plasmodium falciparum alpha-tubulin I gene.
 ACCESSION X15979
 NID 99979
 KEYWORDS alpha-tubulin; tubulin.
 SOURCE malaria parasite.
 ORGANISM Plasmodium falciparum
 Eukaryotae; Mitochondrial eukaryotes; Alveolates; Apicomplexa;
 Haemosporida; Plasmodium.
 REFERENCE 1 (bases 1 to 2648)
 AUTHORS Hyde,J.E.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUL-1989) Hyde J.E., University of Manchester
 Institute of Science and Technology, Dept of Biochemistry and
 Applied Molecular Biology, UMIST P O Box 88, Manchester M60 1QD, UK
 REFERENCE 2 (bases 1 to 2648)
 AUTHORS Holloway,S.P., Sims,P.F., Delves,C.J., Scaife,J.G. and Hyde,J.E.
 TITLE Isolation of alpha-tubulin genes from the human malaria parasite,
 Plasmodium falciparum: sequence analysis of alpha-tubulin
 JOURNAL Mol. Microbiol. 3 (11), 1501-1510 (1989)
 MEDLINE 90136080
 FEATURES
 source Location/Qualifiers
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 /clone="H3.7"
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 SAEKAYHQLSVSETNSAFENPAMMAKCDPRHGKYMACCMLIRGDIVPKDYNAVAT
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 Best Local Similarity 67.3%; Pred. NO. 1.44e-01;
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 QY 4 TAATATAAATTATGTCCTATTATTATAGACACATACATGAAATATCTTAATAAAT 63
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 Db 364 taaaaa-taataaataaaaaaagaaaaaaattacattatt 409
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 RESULT 14
 LOCUS XLPOMCA 9747 bp DNA VRT 02-DEC-1993
 DEFINITION X.laevis POMC-A gene for proopiomelanocortin-A.
 ACCESSION X59370 S35811
 NID 964988
 KEYWORDS colour adaptation; corticotrope (ATCH); melanotrope (a-MSH);
 neuropeptide/opioid; opioid (beta-endorphin); POMC-A gene;
 preprohormone; proopiomelanocortin-A; repetitive element JH12;
 repetitive element Vi; secretion.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
 Pipidae; Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 9747)
 AUTHORS Deen,P.M.T.
 TITLE Direct Submission
 JOURNAL Submitted (03-MAY-1991) P.M.T. Deen, Univ of Nijmegen,
 Toernooiveld, 6525 ED Nijmegen, THE NETHERLANDS
 REFERENCE 2 (bases 1 to 9747)
 AUTHORS Deen,P.M.T., Terwel,D., Bussemakers,M.J.M., Roubos,E.W. and
 Martens,G.J.M.
 TITLE Comparative analysis of the transcriptionally active
 proopiomelanocortin genes A and B of Xenopus laevis
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 9747)
 AUTHORS Deen,P.M., Roubos,E.W. and Martens,G.J.
 TITLE Presence of Vi-transposon-like elements in the proopiomelanocortin
 gene A of Xenopus laevis does not affect gene activity
 JOURNAL Mol. Gen. Genet. 230 (3), 491-493 (1991)
 MEDLINE 92114880
 REFERENCE 4 (bases 1 to 9747)
 AUTHORS Deen,P.M., Bussemakers,M.J., Terwel,D., Roubos,E.W. and
 Martens,G.J.
 TITLE Comparative structural analysis of the transcriptionally active
 proopiomelanocortin genes A and B of Xenopus laevis
 JOURNAL Mol. Biol. Evol. 9 (3), 483-494 (1992)
 MEDLINE 92261311
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REFERENCE  1 (bases 1 to 610)
AUTHORS   Whiting,M.F., Carpenter,J.C., Wheeler,Q.D. and Wheeler,W.C.
TITLE     The Strepsiptera Problem: Phylogeny of the Holometabolous Insect
            Orders Inferred from 18S and 28S Ribosomal DNA Sequences and
            Morphology
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 610)
AUTHORS   Whiting,M.F., Carpenter,J.C., Wheeler,Q.D. and Wheeler,W.C.
TITLE     Direct Submission
JOURNAL    Submitted (25-JUL-1996) Entomology, American Museum of Natural

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MPRELH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
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Listing first 45 summaries

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Statistics: Mean 9.436; Variance 5.783; scale 1.632
Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES						
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1	1280	99.5	1286	24	T42139	Bak-2 gene.
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3	890	69.2	2094	24	T42138	Bak gene.
4	889	69.1	2072	14	Q95492	Human Cdn-1 CDNA.
5	768	59.7	1968	19	T17375	Bcl-1 Y CDNA.
6	753	58.5	5408	14	Q95494	Human Cdn-3 DNA.
c 7	88	6.8	1047	2	Q10572	Human Natriuretic Pep
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c 9	45	3.5	204	1	N31164	Base substituted E.co
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40	25	1.9	198	7	Q42784	Ligand-induced gene,	4.76e-01
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ALIGNMENTS

RESULT 1
ID T42139 standard; CDNA; 1286 BP.
AC T42139;
DT 22-FEB-1997 (first entry)
DE Bak-2 gene.
KW Human; Bak-2; apoptosis; latency; virus replication;
KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
KW protein interactive trapping; virucide; antitumour; diagnostic; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
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PN WO9633416-A1.
PD 24-OCT-1996.
PF 19-APR-1996; U05639.
PR 20-APR-1995; US-426529.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer WC;
DR WPI: 96-485886/48.
DR P-PSDB: W03569.
PT Screening for anti-viral agents - by detecting the ability of an
PT agent to disrupt the interaction of a Bak protein and a viral
PT protein
PS Disclosure; Fig 2: 24pp; English.
CC The sequence encodes Bak-2 protein, which is a bcl-1 homologue which
CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
CC protein, and is capable of modulating apoptosis. The Bak-2 gene is
CC located on human chromosome-20. The protein may be used in
CC complete or partial form, or as an epitope tag fusion protein, in a
CC new virucide drug screening method, which involves combination of
CC Bak-2 protein and a viral protein (e.g. EBV BHRF1), exposure to a
CC test compound, and monitoring for disruption of the interaction,
CC e.g. by co-precipitation, protein interactive trapping or ELISA.
CC Interaction of Bak-2 and viral proteins allows viral replication or

CC latency in the absence of apoptosis. Compounds which inhibit the
CC interaction may be used as virucide, antitumour or diagnostic agents.
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Matches 1286; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Q 1261 GGTCCCCCTCAAGAGTACAGAAGCTT 1287

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AC Q95493;
DT 21-NOV-1995 (first entry)
DE Human Cdn-2 DNA.
KW Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
KW shock; lymphoma; eczema; ss.
OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 3312..3947
FT /tag= a
PN W09515084-A.
PD 08-JUN-1995.
PF 30-NOV-1994; UI3930.
PR 30-NOV-1993; US-160067.
PR 07-OCT-1994; US-320157.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC;
DR WPI; 95-215106/28.
DR P-PSDB: R77877.
PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
PT etc.
PS Claim 6; Fig.5A-H; 66pp; English.
CC Cdn-2 cDNA was isolated from a human placental genomic library
CC using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
CC in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced
CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
CC with Cdn-1 (R77876).
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D 2888 agccactgtccatagttctctatttatagattcttctcttatacaagattattatagcttc 2947
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ID T42138 standard; cDNA; 2094 BP.
AC T42138;
DT 22-FEB-1997 (first entry)
DE Bak gene.
KW Human; Bak; apoptosis; latency; virus replication;
KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
KW protein interactive trapping; virucide; antitumour; diagnostic; ss.
OS Homo sapiens.
FH key Location/Qualifiers
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PN WO9633416-A1.
PD 24-OCT-1996.
PF 19-APR-1996; U05639.
PR 20-APR-1995; US-426529.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC;
DR WPI; 96-485886/48.
DR P-PSDB; W03668.
PT Screening for anti-viral agents - by detecting the ability of an
PT agent to disrupt the interaction of a Bak protein and a viral
PT protein
PS Disclosure; Fig 1; 24pp; English.
CC The sequence encodes Bak protein, which is a bcl-1 homologue which
CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
CC protein, and is capable of modulating apoptosis. The Bak gene is
CC located on human chromosome-6 at 6p21-23. The protein may be used
CC in complete or partial form, or as an epitope tag fusion protein,
CC in a new virucide drug screening method, which involves combination
CC of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a
CC test compound, and monitoring for disruption of the interaction,
CC e.g. by co-precipitation, protein interactive trapping or ELISA.
CC Interaction of Bak and viral proteins allows viral replication or
CC latency in the absence of apoptosis. Compounds which inhibit the
CC interaction may be used as virucide, antitumour or diagnostic agents.
CC Sequence 2094 BP; 410 A; 608 C; 606 G; 470 T;
SQ
```

Query Match 69.2%; Score 890; DB 24; Length 2094;
Best Local Similarity 98.2%; Pred. No. 0.00e+00;
Matches 917; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

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Db 13 gggacaagtaaaaggctacatccagatccggggaatgactgacgcccattctcggaaact 72
QY 355 GGGACAAGTAAAGGCTACATCCAGATCTGGGAATGCACTGACGCCCATCTCTGGAAACT 414
Db 73 gggctccactcagccccctgggagcagcagcgcgagccctcgg-acctccatctccac 131
QY 415 GGGCTCCACTCAGCCCCCTGGGACACAGCCGCCACCCCTCGGGACCTCCATCTCCAC 474
Db 132 cctgctgagccaccccggttgggcccaggtatcccgaggctgattcccgctcctccactgag 191
QY 475 CTTGCTGAGCCACCCCGGTTGGGCCAGGATCCCGGACAGCTCCCTCCAGGAGTGGGAGCCT 534
Db 192 acctgaaaaatgcttcgggggaagcccgaggtcctcccgagggagtgctccactgag 251
QY 535 ACCTGAAAAATGGCTTCGGGCGCAGGCCAGGCTCCTCCAGGAGTGGGAGCCT 594
Db 252 gccctgcctcctctcttgaggagcaggtagccacagacacagaggggttttccgcagc 311
QY 595 GCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCCGACAGACACAGAGAGGTTTTCGGCAGC 654
Db 312 taogttttttacogccatcagcaggaagaggtgaaaggggtggtggtgcccctgcgcgac 371
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655 TACGTTTTTACCACCATCAGCAGGAACAGGAGGCTGAAGGGGGGCTGCCCTCGCGAC 714
Db 372 ccagagatggtcacctctcctcaacctagcagcaccatggggcagggtggagcgcag 431
Qy 715 CCAGAGATGGTCACCTTACCTCTCAACCTAGCAGCACCATTGGGGCAGGTGGGACGAC 774
Db 432 ctgcccacatcgcgggagcagatcaaccgagcgtatgactcagaggttccagaccatgttg 491
Qy 775 CTCGCCATCATTTGGGACGACATCAACGACGCTATGACTCAGAGTTCACAGACCATGTTG 834
Db 492 cagcacctgcagccacagcagagagaaagcgtatgactcagaggttccacaaagattggcaccagc 551
Qy 835 CAGCACCTGCAGCCACAGGCGCAGAAATGCCCTATGAGTACTTCAACCAAGATTGCCCTCCAGC 894
Db 552 ctgtttgagagtgcatcaaatgtggggccgtgtggtgctctcttctggtcttcggctacagct 611
Qy 895 CTGTTTGAGAGTGGCATCAATTTGGGGCGGTGTGTGGCTCTTCTGGGCTTCAGTACCGT 954
Db 612 ctggccctacacgtctaccagcatggcctgactggtcttccctaggccaggtgaccgccttc 671
Qy 955 CTGGCCCTACACATCTACCACGCTGGCTGACTGGCTTCTTGGGCCAGGTGACCCGCTTT 1014
Db 672 gtgctgactcactcgtcgtcatcactgcatgctgctgctgctgctgctgctgctgctgctg 731
Qy 1015 GTGTTGAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
Db 732 gtgcagccctgaactgtgggcaatggttccatcctcctcctcctcctcctcctcctcctcct 791
Qy 1075 GTGGCAGCCCTGAATTTGGGCAATTTGGGCAATTTGGGCAATTTGGGCAATTTGGGCAAT 1134
Db 792 gtctgttggggccagttgtgtgtacgaagattcttcaaatcatgactcccaagggtgccc 851
Qy 1135 GTTCTGTGGCCAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1194
Db 852 ttgtgggtccgggttcagaccctcctcctcctcctcctcctcctcctcctcctcctcctcct 911
Qy 1195 TTGGGTGCCAGTTTCAGACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
Db 912 cttcaggggtccccctcaagagacagaagcctt 945
Qy 1255 -TTGAGGGTCCCCCTCAAGAGTACAGAAGCTT 1287
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RESULT 4

```
ID Q95492 standard; cDNA; 2072 BP.
AC Q95492; 1995 (first entry)
DE Human Cdn-1 cDNA.
KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
KW shock; lymphoma; eczema; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 188..903
FT /tag= a
PN W09515084-A.
PD 08-JUN-1995.
PF 30-NOV-1994; U13930.
PR 30-NOV-1993; US-160067.
PR 07-OCT-1994; US-320157.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Klefer MC;
DR WPI: 95-215106/28.
DR P-PSDB: R77876.
DR New nucleic acid sequences encoding Cdn apoptosis modulators - and
CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
CC previously isolated clone as probe. Recombinant Cdn-1 was produced
CC in Sf9 and human colon adenocarcinoma HT29 cells. Expression of
```

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CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
CC survival in response to anti-Fas-mediated apoptosis.
SQ Sequence 2072 BP; 404 A; 603 C; 598 G; 467 T;

Query Match 69.1%; Score 889; DB 14; Length 2072;
Best Local Similarity 98.2%; Pred. No. 0.00e+00;
Matches 916; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

Db 1 ggacaaataaggctacatccagatgccgggaatgcaactgacgcccattctggaaactg 60
Qy 356 GGACAAGTAAGGCTACATCCAGATGCTGGGAATGCACTACGCCCATTTCTTGGAAACTG 415
Db 61 ggtcccaactcagccctgggagcagcagcgccagccctcgg-actcactatccacc 119
Qy 416 GGCTCCCACTCAGCCCTGGGAGCAGCGCGCAGCCCTTCGGGACCTTCATCTCCACC 475
Db 120 ctgctgagccaccgggtgtgggcccagatccccggcaggtgatccccctcctccactgaga 179
Qy 476 CTGCTGAGCCACCGGGTGTGGCCAGGATCCGGCAGGCTGATCCCGTCTCCACTGAGA 535
Db 180 cctgaaaaatggtctcggggcaaggcccaggtcctcccagcagagtagtgcggagagcgtg 239
Qy 536 CCTGAAAAATGGCTTCGGGGCAAGGCCCATGCTCTCCAGGCAGAGTGGGAGAGGCTG 595
Db 240 cctgtccctctgtcttgagagcaggtagccagagcacagagaggttttccgcagct 299
Qy 596 CCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCCAAGGACACAGAGAGGTTTTCGCCAGCT 655
Db 300 acgtttttaccgscatcagcaggaacagaggtgaggtgaggtggtggtggtggtggtggtggt 359
Qy 656 ACGTTTTTTACCACCATCAGCAGGAACAGAGGCTGAAGGGGGCGCTGCCCTCCGACC 715
Db 360 cagagatggtcacttaccctctgcaacctagcagcacacatggggcaggtgggagcagc 419
Qy 716 CAGAGATGGTCACTTACCTCTGCAACCTAGCAGCACCATTGGGCAAGTGGGAGCGGACG 775
Db 420 tcgcatcatctcgggagcagacatcaacgacgctatgactcagaggttccagaccatgtgc 479
Qy 776 TCGGCATCATTTGGGACGACATCAACCGACGCTATGACTCAGAGTTCCAGACCATGTTGC 835
Db 480 agcacctgcagccacgcagagagaatgcctatgacttaccacaaagattgcccaccgacc 539
Qy 836 AGCACCTGCAGCCACGCGCAGAGAAATGCCATGATGATGATTTCAACCAAGATTGCCCTCCAG 895
Db 540 tgtttgagagtgcatacaattggggccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 599
Qy 896 TGTGTGAGAGTGGCATCAATTTGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
Db 600 tggccctacacgtctcagcagcgtgactgcttccctagcagcaggtgacccgcttcg 659
Qy 956 TGGCCCTACACATCTACAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1015
Db 660 tggctgacttcagtcgcatcactgcattgcccgggtgattgacacagaggggtggtggtggtggt 719
Qy 1016 TGTGTGACTTCATGCTGCATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
Db 720 tggcagccctgaacttgggcaaatggtcccatcctgacacgtgctgtgtgtgtgtgtgtgtgtgt 779
Qy 1076 TGGCAGCCCTGAACCTTGGGCAATTTGGTCCCATCTCCATCTCCATCTCCATCTCCATCTCC 1135
Db 780 ttctgttggggcagttgtgtgtacgaagattcttcaaatcatgactccccaaaggggtgcct 839
Qy 1136 TTCGTTGGGCCAGTTTGTGTGTCGAAGATTCTTCAATCATGACTCCCCAAGGGTGCCTT 1195
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Qy 1196 TGGGGTCCCACTTCAGACCCCTGCTGGACTTAAGCGAAGTCTTTGCTTCTCTGCTCC- 1254
Db 900 ttgagaggtccccctcaagagtagacagaagcctt 932
Qy 1255 TTGAGGGTCCCCCTCAAGAGTACAGAAGCTT 1287
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Qy	497	GCCAGGATCCCGGAGGCTGATCCCGTCTCTCCACTGAGACCTGAAAAATGGCTTCGGGGC	556
Db	1678	aaggccacgggctccacgacgagagtcggaagcctgcctgcctctctctcagg	1737
Qy	557	AAGGCCAGGTCTCTCCAGCAGGAGTGGGAGAGCTGCCCCTGCTTCTCTGAGG	616
Db	1738	agcaggtagccaggacatggag-ggttttcgcagctaaqgtttttaccaccatcagc	1796
Qy	617	AGCAGGTAGCCAGGACACAGAGGAGGTTTCCGCAGCTACGTTTATACCACTCAGC	676
Db	1797	agaaacaggaggctgaaggggggcgcgccttcgcagaccagagatggtcaccttgcgcc	1856
Qy	677	AGGAACAGGAGGCTGAAGGGGGCGCTGCCCCCTGCCAGCCAGAGATGCTACCTTACCTC	736
Db	1857	tcaaacctagcagcacacatggggcaggctggggacgcagctgcacatcacagg-accaca	1915
Qy	737	TGCAACCTAGCACACCATGGGGCAGTGGGACGGCAGCTGCCATCATTGGGACGACA	796
Db	1916	tcaacgggcactatgacttcggagttccagacacatgctgcagcaactgcagccacagcca	1975
Qy	797	TCAACCGACGCTATGACT-CAGAGTTCCAGACCATGTTGCAGCACTGCACGCCACCGCA	855
Db	1976	gagaacgctcacagTacttcaccaagaTcgctccagcctgttgagagtggtcatcaac	2035
Qy	856	GAGATGCCATACAGTACTTCCACCAAGATTGCTCCAGCTGTTTGAGAGTGGCATCAAT	915
Db	2036	cggggcgcgtgggtgctctctgggcttcggctaccgctcgtgtctcatgctctacag	2095
Qy	916	TGGGGCGTGTGTGGCTCTCTGGGCTTCAGTACCGTTCGGCCCTACATCTACACG	975
Db	2096	cacggttgactggctctctgggctgttgaccgcctgttggt---cttcagtctcaa	2152
Qy	976	CGTGGCCTGACTGGCTTCTTGGGCCAGGTGACCCGCTTGTGGTGGACTTTCATGCTCAT	1035
Db	2153	caaggcatcgccgggtgatctctgcagagggcgcgctgggtggcagccctggaacttgggc	2212
Qy	1036	CAC TGCA TTTCCCGGTGGAT TGCACAGAGGGGTGGCTGGTGCGACGCCCTGAATTTGGC	1095
Db	2213	aatagtcceactctgaactgctggtgtgtgtgggtgtgttctctgctggggcagattgtg	2272
Qy	1096	AATGGTCCCATCTGAACGCTGGTGGTTCTTGGGTGGTGTCTGTGGGGCACTTTGTG	1155
Db	2273	qtaagaagatcttctcaaatcatgactccccaggggtgctctttggggtccccagctgacc	2332
Qy	1156	GTACGAGATCTTCAAAATCATGACTCCCAAGGGTG-CCTTTGGGTGCCAGTTCAGACC	1214
Db	2333	ctgctctggacttaagccaaagtcttttgccttccccactcctcttgagggtcaccccttca	2392
Qy	1215	CTGCTCTGGACTTAAGCGAAGTCTTTGGCTTCTCTGCTCC-TTGCAGGG-TCCCCCTCA	1272
Db	2393	aaagtacagaagct 2406	
Qy	1273	AGAGTACAGAAGCT 1286	

RESULT 7

RESULT	REFERENCE
ID	Q10572 standard; DNA: 1047 BP.

AC Q10572;
Q10572 SCANDIA, DNR, 1047 BF.

DT 09-APR-1991 (first entry)

DE Human Natriuretic Peptide Receptor

KW NPRB; ANP; BNP; CNP; kidney failure
KW hyperaldosteronism: α1-antagonists

NW hyperaldosteronism; glaucoma;
OS Homo sapiens.

FH	Key	Location/Quali
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FT	Peptide	1.22
1.22	1.22	1.22

FT	/label=	signal sequence
FT	12	protein

FT	protein	12
FT	/label= mature NPBR	

FT	Domain	23..455
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FT	/label= extracellular domain
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FT	/note=	"binds natriuretic pept
FT	Domain	456 456

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FT domain 456..456
FT /label= transmembrane domain
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11/11/2017 11:11 AM

FT	Domain	479..1047
FT	/label=	cytoplasmic domain
FT	/note=	"GC and protlen kinase activity"

Query Match 6.8%; Score 88; DB 2; Length 1047;

Best Local Similarity 8.3%; Pred. No. 5.85e-38;

Matches 61; **Conservative** 215; **Mismatches** 450; **Indels**

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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[illegible]

Cp 1287 AAGCTTCTGTACTCTTTGAGGGGGACCCCTGCACCGCAGCACACACATTCCTT 1329

CP 128/ AAGCTTCTGTACTCTTGAGGGGGGACCTTGC AAGGAGCAGAGAAGGC AAAGACTTCGCCT 1228

Db 359 ndgnrnvnkmgrryhgvtnvmdknnrdnrntdnvnwamqndnsqdnnnnaahysqanknn 418

[illegible]

Cp 1227 AAGTCCAGGCAGGGGT-CTGAACCTGGGACCCCAAAGGCACCCCTTGGGAGTCATG-ATTG 1170

[illegible]

Db 419 wwtgrnnnwkgannsdnnncandndddnsdcktnnstnanvagtntnmmgvssnnn 478

Cp 1169 AAGAAATCTTCGTACCAAAACTGGCCCAACGACACACCCACACCGCACC

CP 1189 AAGAAATCTTCGTACCAACAACCTGGCCCAACAGAAACCAACCCAGAACCAACGACGTTCTTTT

Db 479 rknmnnknnsasnmwrrnrwnnnnnnqnsnrvhkqagsrntnsnrgssvqssmntabqkyppna 538

Число	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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Cp 1109 AGGATGGGACCATTGCCCAAGTTCAGGGCTGCCACCCAGCCACCCCTCTGTGCAATCCAC 1050

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FT misc_feature 19..69
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FT misc_feature 19..69
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CC occurred singularly in any given mutant.
CC See also P80575.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match 3.1%; Score 40; DB 1; Length 204;
Best Local Similarity 12.9%; Pred. No. 8.16e-09;
Matches 13; Conservative 53; Mismatches 34; Indels 1; Gaps 1;

Db 95 rrmrnbvdyrnrsdaawccyrsvkycynachdhhyvbybbbnvnhnnmcnc 154
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281 AACATCATTTAAAAAACATTTTTTGGCTGGCACCTGATCATCCTGGAGTCGCGGGTC 340

Db 155 cbnvhcnvhnbnhrnwayvrhdarrddvcvchcogat 195
! :
QY 341 CCTCAGGCTGC-ACAGGGACAAGTAAGGCTACATCCAGAT 380

RESULT 13

ID Q70468 standard; DNA; 114 BP.

AC Q70468;

DE Generic DNA sequence to generate a random TSAR peptide library.

KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;

KW effector domain; concatenated heterofunctional protein; linker;

KW direct; rapid; detection; screening; treatment; generic; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT misc feature 55..60

FT /*tag= a

FT /note= "this sequence represents 'Z'; Z can be a

FT sequence of 6, 9 or 12 nucleotides (see

FT comments)"

FT FT

PD W09418318-A.

PN 18-AUG-1994.

PE 01-FEB-1994; U00977.

PR 01-FEB-1993; US-013416.

PR 30-DEC-1993; US-176500.

PR 31-JAN-1994; US-189331.

PA (UYNC-) UNIV NORTH CAROLINA.

PI Fowlkes DM, Kay BK;

P1 WPI: 94-279739/34.

DR P-PGDB; R65154.

PT Identifying proteins or peptide(s) which bind a ligand - by

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

PS Disclosure; Page 35; 255pp; English.

SC Q70468 is a generic DNA sequence used to generate random TSAR (Totally

CC Synthetic Affinity Reagents) peptides.This generic formula can also be

CC represented as follows: X(NNNB)ll(TGC)(NNB)6z(NNB)7(TGC)(NNB)l0Y. X

CC and Y are flanking restriction sites (X is not the same as Y) that are

CC not specified further. Other generic sequences are shown in Q70466-68.

CC Other specific peptides generated by these generic sequences are shown in

CC Q65151-54. TSARS are concatenated heterofunctional proteins or peptides,

CC comprising at least two functional regions - a binding domain with

CC affinity for a ligand and a second effector peptide portion that is

CC chemically or biologically active.They may further comprise a linker

CC peptide between the 2 domains.The oligonucleotides are also designed so

CC that the expressed peptide contains 2 or 4 cysteine residues positioned

CC in, or flanking, the unpredicted or variant residues. These residues

CC confer some degree of conformational rigidity to the peptides. The TSARS

CC or comps. comprising a TSAR binding domain can be used in vivo to

CC deliver a chemically or biologically active moiety, eg. metal ion,

CC radioisotope, peptide, toxin or enzyme, to the specific target or on the

CC cell. They can also replace the function of macromolecules, eg.

CC monoclonal or polyclonal antibodies and therefore circumvent the need

CC for complex methods of hybridoma formation or in vivo antibody

CC production. The TSARS are easily characterised and have designed activity

CC allowing direct and rapid detection in a screening process.

CC Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

SQ

Query Match 2.8%; Score 36; DB 12; Length 114;
Best Local Similarity 3.6%; Pred. NO. 1.26e-06;
Matches 4; Conservative 34; Mismatches 74; Indels 0; Gaps 0;

QY 968 TCTACACGGCTGCTGACTGGCTTCTCTGGCCAGCTGACCCGCTTTG 1017

RESULT 15
 ID Q70467 standard; DNA; 114 BP.
 AC Q70467.
 DT 05-APR-1995 (first entry)
 DE Generic DNA sequence to generate a random TSAR peptide library.
 KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
 KW effector domain; concatenated heterofunctional protein; linker;
 KW direct; rapid; detection; screening; treatment; generic; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_feature 55..60
 FT /*tag= a
 FT /note= "this sequence represents '2'; Z can be a
 FT sequence of 6, 9 or 12 nucleotides (see
 FT comments)"
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 PD 18-AUG-1994. U00977.
 PE 01-FEB-1994; US-013416.
 PR 01-FEB-1993; US-176500.
 PR 30-DEC-1993; US-176500.
 PR 31-JAN-1994; US-189331.
 PA (UINC-) UNIV NORTH CAROLINA.
 PI Fowlkes DM, Kay BK;
 DR WPI: 94-279739/34.
 DR P-PSDB; R65153.
 PT Identifying proteins or peptide(s) which bind a ligand - by
 PT screening a recombinant vector library expressing fusion proteins
 PT comprising a binding domain and an effector domain
 PS Disclosure; Page 35; 253pp; English.
 CC Q70467 is a generic DNA sequence used to generate random TSAR (Totally
 CC Synthetic Affinity Reagents) peptides. This generic formula can also be
 CC represented as follows: X(NNB)16(TGC)(NNB)16(TGC)(NNB)1Y. X
 CC and Y are flanking restriction sites (X is not the same as Y) that are
 CC not specified further. Other generic sequences are shown in Q70466-68.
 CC Other specific peptides generated by these generic sequences are shown in
 CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
 CC comprising at least two functional regions - a binding domain with
 CC affinity for a ligand and a second effector peptide portion that is
 CC chemically or biologically active. They may further comprise a linker
 CC peptide between the 2 domains. The oligonucleotides are also designed so
 CC that the expressed peptide contains 2 or 4 cysteine residues positioned
 CC in, or flanking, the unpredicted or variant residues. These residues
 CC confer some degree of conformational rigidity to the peptides. The TSARs
 CC or compens. comprising a TSAR binding domain can be used in vivo to
 CC deliver a chemically or biologically active moiety, eg. metal ion,
 CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
 CC cell. They can also replace the function of macromolecules, eg.
 CC monoclonal or polyclonal antibodies and therefore circumvent the need for
 CC complex methods of hybridoma formation or in vivo antibody production.
 CC The TSARs are easily characterised and have designed activity allowing
 CC direct and rapid detection in a screening process.
 SQ Sequence 114 BP; 2 A; 2 C; 2 G; 2 T;
 Query Match 2.8%; Score 36; DB 12; Length 114;
 Best Local Similarity 4.5%; Pred. No. 1.26e-06;
 Matches 5; Conservative 33; Mismatches 74; Indels 0; Gaps 0;
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 QY 933 TCTTCTGGGCTTCAGCTACGCTGCGCTTACACATCTACACGCGTGGCTGACTGGCTT 992
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Search completed: Thu Aug 21 13:23:47 1997
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
C 1	272	21.2	497	155	AA016399	mg88g02.r1 Soares mou	0.00e+00
C 2	273	21.1	303	85	H56462	yt87a12.r1 Homo sapie	0.00e+00
C 3	254	19.7	545	153	W42014	mb16g04.r1 Soares mou	0.00e+00
C 4	232	18.0	442	138	AA049970	mj39b01.r1 Soares mou	0.00e+00
C 5	72	5.6	292	138	AA049828	mj09a09.r1 Soares mou	4.27e-87
C 6	72	5.6	361	139	AA050569	mjl6b12.r1 Soares mou	4.27e-87
C 7	60	4.7	232	133	N83998	KK4271f.Homo sapiens	3.44e-64
C 8	46	3.6	270	175	W82028	mf02e01.r1 Soares mou	7.53e-39
C 9	39	3.0	320	186	AA139013	mr04a06.r1 Soares mou	5.11e-27
C 10	31	2.4	279	82	H31840	EST106323 Rattus sp.	1.48e-14
C 11	24	1.9	266	129	HSC07H082	H. sapiens partial CD	4.59e-05
C 12	24	1.9	337	109	HSC3LCO12	H. sapiens partial CD	4.59e-05
C 13	24	1.9	358	133	N92010	za21a11.r1 Homo sapie	4.59e-05
C 14	24	1.9	395	54	H03526	yj37c07.r1 Homo sapie	4.59e-05
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C 25	24	1.9	478	110	HUM403H04B	Human fetal brain CDN	4.59e-05
C 26	24	1.9	480	136	AA0011756	zh84b09.s1 Soares fet	4.59e-05
C 27	24	1.9	487	125	W74617	zd77e01.s1 Soares fet	4.59e-05
C 28	25	1.9	500	61	H15311	ym28b07.r1 Homo sapie	2.60e-06
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C 30	23	1.8	251	48	HUM250H12B	Human aorta cDNA 5'-e	7.34e-04
C 31	23	1.8	300	129	HSC0M8041	H. sapiens partial CD	7.34e-04
C 32	23	1.8	301	186	AA138853	mr03a06.r1 Soares mou	7.34e-04
C 33	23	1.8	317	78	R97647	yy59c09.s1 Homo sapie	7.34e-04
C 34	23	1.8	317	29	R67853	yl28d10.s1 Homo sapie	7.34e-04
C 35	23	1.8	340	107	HSC2SG051	H. sapiens partial CD	7.34e-04
C 36	23	1.8	368	194	AA169681	zo92f06.r1 Stragatene	7.34e-04
C 37	23	1.8	372	18	T50771	yb88e05.s1 Homo sapie	7.34e-04
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C 39	23	1.8	378	197	AA173916	zp01b08.s1 Stragatene	7.34e-04
C 40	23	1.8	391	103	N72841	za03b02.s1 Homo sapie	7.34e-04
C 41	23	1.8	391	115	W17230	zb14a04.r1 Soares fet	7.34e-04
C 42	23	1.8	412	159	AA036957	zk32a09.s1 Soares pre	7.34e-04
C 43	23	1.8	445	174	W80365	zd82a03.s1 Soares fet	7.34e-04
C 44	23	1.8	490	138	AA046492	zk72c08.s1 Soares pre	7.34e-04
C 45	23	1.8	523	161	AA054723	zk68d08.s1 Soares pre	7.34e-04

ALIGNMENTS

RESULT 1

LOCUS	AA016399	497 bp	mRNA
DEFINITION	mg88g02.r1	soares mouse embryo	

clone 4A114 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X_L

ACCESSION
AA016399
BCD X. 1.

NID g1478767

Db 61 gagagcaggtagcccccagacagagagggttttccgcagctacgtttttttaccaccat 120
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Db 121 cagcagaaacagagaggtgaagggcggtgctgcagcnc-gaccagagatggtcacctta 179
 QY 673 CACGAGAAACAGAGGCTGAAGGGCGGTGCCCCCTCCGACCCAGAGATGGTCACCTTA 732

Db 180 cctctgcaacctagcagcaccatggggcaggtgggagcgagctcgccatcattggggac 239
 QY 733 CCCTCTCAACTAGCAGCACCATGGGCGAGGTGGGACGAGCTCGGCATCATTTGGGAC 792

Db 240 gacataaacagcagctatgactcagagttccagaccatgttncagcaccctgcagtccac 299
 QY 793 GACATCAACGAGCGTATGACTCAGAGTTCAGACCATGTTGCAGCACCTGCGAG-CCCAC 851

Db 300 ggca 303
 QY 852 GGCA 855

RESULT 3
 LOCUS W42014 545 bp mRNA EST 11-SEP-1996
 DEFINITION mb16g04.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 329622 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. ;
 ACCESSION W42014
 NID 91326554
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 545)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennan,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:211022
 Possible reversed clone: similarity on wrong strand
 Seq primer: ETPrimer
 High quality sequence stop: 411.
 Location/Qualifiers
 1..545
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 /note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
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mrna /lab_host="DH10B (ampicillin resistant)"
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 Matches 384; Conservative 0; Mismatches 100; Indels 5; Gaps 5;

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Db 89 aagaatctgtgtaccaggaattggcccaacagacacacacacacacacacacacacacac 148
 Cp 1169 AAGAAATCTTCGTACCAAACTGGCCCAACAGAACACACACCCAGAACCCACGACGCTTC 1110

Db 149 aggatgggactctagaaaaattcagggtcggccacccacccacccctctctgtgcattcat 208
 Cp 1109 AGGATGGGACCATTGCCAAAGTTCAGGGCTGCCACCCAGCCACCCCTCTGTGAAATCCAC 1050

Db 209 ctggcagatgaatgacgtatgatcagcccaaaaagcaggtcacctggcccagaag 268
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Db 269 ccggtcaaacacacgcgtggtacgtacagggccagacggttagccaaagccagagagcc 328
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Db 329 accacggcccccagctgacacactttaaataaggctgagggcagctcttggggaagagt 388
 Cp 929 ACCACAGCGGCCCAATGATGCCACTCTCAACAGGGCTGGAGGCAATCTTGGTGAAGTAC 870

Db 389 tcgtaggcattccggctggtggaagcttcttagtagattctggaactctgtgtcg 448
 Cp 869 TCATAGGCAATCTCTGCCGCGGCTGACAGTGTGCAACATGCTCTGGAACCTGAGTCA 810

Db 449 ta-cgcgggttaataca-ctccgatgagagcagctgcccacc-acgttgaccacagatg 505
 Cp 809 TAGCGTCGGTTGATGTCGTCCCAATGATGGCGAGCTGCCGCTGCCACCTGCCCATGGTG 750

Db 506 ctggtgggt 514
 Cp 749 CTGCTAGGT 741

RESULT 4
 LOCUS AA049970 446 bp mRNA EST 09-SEP-1996
 DEFINITION mj39b01.r1 Soares mouse embryo NbMEL3.5 14.5 Mus musculus cDNA clone 478441 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. ;
 ACCESSION AA049970
 NID g1529641
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 446)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennan,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800

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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289185
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 319.
Location/Qualifiers
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/strain="C57BL/6J"
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TGTACCAATCTAAGTGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
3' ], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru KO, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
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mRNA
BASE COUNT
ORIGIN

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Db	191	gtcgtatcccatctggcgatgtaatgtatgcagtatgatatacagccaaaagcaggtcacct	250	
Cp	1060	GTGCATCCACCGGGCAATGCAGTGATGCAGTGAAGTCCACCAAAAGCGGGTCACCT	1001	
Db	251	ggcccagggaagccggtctaaaccacgcgtggtagacgtacagggccagacaggtagccaaagc	310	
Cp	1000	GGCCAGGAAGCCAGTCAGGCCACGCTGGTGTAGTGTGTAGGGCCAGACGGTAGCTGAAGC	941	
Db	311	ccaggagagccacacagcggcccccagctgtatgcactctttaataggctggaggcgatct	370	
Cp	940	CCAGAAGAGCCACACAGCGCCCAATTGTATGGCACTCTCAAAACAGCGCTGGAGGCAATCT	881	
Db	371	tggtgaagagtctgtaggcatttcccgctgtggcctgaagctttctagttaaatcttca	430	
Cp	880	TGCTGAAGTACTCATAGGCATTCTCTCGCGTGGGCTGCAGGTGCTCTCACATGGTCTGGA	821	
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RESULT	AA049828	292 bp	mRNA	
LOCUS	mJ08a09.r1 Soares mouse embryo NBME13.5	14.5	Mus musculus CDNA	
DEFINITION	clone J75576 5'			
ACCESSION	AA049828			
NID	G1529499			

KEYWORDS	EST.
SOURCE	house mouse
ORGANISM	Mus musculus
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 292)
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and Waterston,R.
TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:286320 Seq primer: -28M13 rev2 from Amersham.

FEATURES
SOURCE

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/strain="C57BL/6J"
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was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTCGGAGCGCGCGGAATTTTTTTTTTTTTTTT
T 3'] on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
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Db	241	cttcgaaagtacgttttttaccctccaccagcaggaaacagggagaccagggg	292	
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LOCUS					
DEFINITION		mj16b12.r1 Soares mouse embryo	NBWE13.5	14.5	Mus musculus cDNA
		Clone 476255	5'		

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ACCESSION AA050569
NID q1530241
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
          Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
          Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
          Theising,B., Wylie,T., Lennan,G., Soares,B., Wilson,R. and
          Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
          WashU-HMI Mouse EST Project
          Washington University School of MedicineP
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: mouseest@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          MGI:286999
          Seq primer: -28M13 rev2 from Amersham.
          Location/Qualifiers
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              /organism="Mus musculus"
              /strain="C57BL/6J"
              /note="vector: p7T3D-Pac (Pharmacia) with a modified
              polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
              was primed with a Not I - oligo(dT) primer [5',
              TGTACCACTGTAAGTGGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTT
              T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
              14.5dpc embryos [total RNA provided by Minoru KO, Wayne
              State Univ., from 2 ]; double-stranded cDNA was ligated to
              Eco RI adaptors (Pharmacia), digested with Not I and
              cloned into the Not I and Eco RI sites of the modified
              pT73 vector. Library went through one round of
              normalization, and was constructed by Bento Soares and
              M.Fatima Bonaldo."
              /clone="476255"
              /clone_lib="Soares mouse embryo NDME13.5 14.5"
              /sex="unknown"
              /tissue_type="embryo"
              /dev_stage="13.5-14.5dpc total fetus"
              /lab_host="DH10B"
              <1..>361

BASE COUNT 87 a 108 c 103 g 63 t
ORIGIN
Query Match 5.6%; Score 72; DB 139; Length 361;
Best Local Similarity 79.7%; Pred. No. 4.27e-87;
Matches 137; Conservative 0; Mismatches 29; Indels 6; Gaps 4;

Db 196 ctccaccagacctgaaatggcatctggacagcagggtcccccgaaggtggctg 255
Qy 525 CTCACCTGAGACCTGAAATATGGCTTCGGGGCAAGCGCCGAGGTCTCCGACGAGGAGTG 584

Db 256 cgatgagtc--ccc-gtcc-c--cttctgaacagcagggtgcccagcagcagagaggt 309
Qy 595 CGGAGAGCTGCCCTGCCCTCTGCTCTCTGAGGAGGAGGTAGCCAGCAGACAGAGAGGT 644

Db 310 ctttcgaagctacgttttttaacctccaccagcaggaacagagagcccgagg 361
Qy 645 TTTCGGCAGCTACGTTTATACCATCAGCAGGAACAGGAGGCTGAAGGG 696

RESULT 7 N83998 232 bp mRNA EST 01-APR-1996
LOCUS WashU-HMI Mouse EST Project

DEFINITION KK4271F Homo sapiens cDNA clone KK4271 5' similar to BAK FOR BCL-2
HOMOLOGUE.
ACCESSION N83998
NID g1259623
KEYWORDS EST.
SOURCE human clone-KK4271 primer-GAATTAACCTCCTAAAGGG library-Fetal
heart. Lambda ZAP Express vector-Lambda ZAP Express host-E. coli
XLI-Blue RsiteI-EcoRI Ksite2-XhoI mRNA was purified from human
fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo
dT adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into predigested
lambda ZAP Express.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 232)
TITLE cDNAs from fetal heart
JOURNAL Unpublished (1996)
COMMENT Contact: Liew CC
          Molecular Cardiology
          University of Toronto
          Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
          Tel: 4169788758
          Fax: 4169785650
          Email: liewcc@utcc.utoronto.ca.
          Location/Qualifiers
            1..232
              /organism="Homo sapiens"
              /clone="KK4271"
              <1..>232

BASE COUNT 52 a 69 c 57 g 54 t
ORIGIN
Query Match 4.7%; Score 60; DB 133; Length 232;
Best Local Similarity 96.9%; Pred. No. 3.44e-64;
Matches 62; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 87 tcagagagcaggttagccacagcagcagagaggtttcccgacgacgtttttaccgc 146
Qy 610 TCTGAGGACGAGGTAGCCGAGGACACAGAGGAGGTTTCCGACGCTAGCTTTTACCAC 669

Db 147 catc 150
Qy 670 CATC 673

RESULT 8 W82028 270 bp mRNA EST 12-SEP-1996
LOCUS mf02e01.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 403896
DEFINITION 5.
ACCESSION W82028
NID g1393105
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 270)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
          Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
          Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
          Theising,B., Wylie,T., Lennan,G., Soares,B., Wilson,R. and
          Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
          WashU-HMI Mouse EST Project

```

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:247664

Seq primer: -28M13 rev2 from Amersham.

FEATURES

source
 Location/Qualifiers
 1..270
 /organism="Mus musculus"
 /note="Vector: pT73D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTACCAATCTGAAGTGGGCGCGCATTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."
 /clone="403896"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 <1..>270

BASE COUNT 61 a 83 c 74 g 52 t
 ORIGIN

Query Match 3.6%; Score 46; DB 175; Length 270;
 Best Local Similarity 76.7%; Pred. No. 7.53e-39;
 Matches 102; Conservative 0; Mismatches 26; Indels 5; Gaps 4;

Db 143 ctccaccagacctgaaatggcatctggacaggaccaggtcccccgaagggtg-9t- 200

QY 525 CTCACACTGAGACCTGAAATGGTTCGGGCGGACGGCGCGTCTCCAGCGAGGAGTG 584

Db 201 ctgcgatgagctcccgctcc-c-cttctgaacagcaggttcccgacacacagagaggt 257

QY 585 CGGAGAGCCCTCCCTGCGCTGCTGAGGACAGTAGTCCCGACACAGAGAGGT 644

Db 258 ctttcgaagctac 270

QY 645 TTCCGCGAGCTAC 657

RESULT 9 AA139013 320 bp mRNA EST 02-DEC-1996
 LOCUS mr04a06.r1 Soares mouse 3NbMS Mus musculus cDNA clone 596434 5,
 DEFINITION similar to TR:G595926 G595926 BAK-2 PROTEIN. ;.
 ACCESSION AA139013
 NID g1701240
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Mus.

REFERENCE 1 (bases 1 to 320)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lannon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:361866

Seq primer: -28M13 rev2 from Amersham.

FEATURES

source
 Location/Qualifiers
 1..320
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; [5',
 TGTACCAATCTGAAGTGGGCGCGCGTGTGTGTGTGTGTGTGTGT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT73 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through
 three rounds of normalization, and was constructed by
 Bento Soares and M.Fatima Bonaldo."
 /clone="596434"
 /clone_lib="Soares mouse 3NbMS"
 /sex="male"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 <1..>320

BASE COUNT 68 a 92 c 96 g 64 t
 ORIGIN

Query Match 3.0%; Score 39; DB 186; Length 320;
 Best Local Similarity 84.2%; Pred. No. 5.11e-27;
 Matches 48; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 264 ccgtccctctgaacagcaggttcccgacacacagagaggtcttccaagctac 320

QY 601 CCCTCTCTCTTGAGGACAGGTAGCCCGACACAGAGAGGTTTCCGCGAGCTAC 657

RESULT 10 H31840 279 bp mRNA EST 08-SEP-1995
 LOCUS EST106323 Rattus sp. cDNA 5' end.
 DEFINITION H31840
 ACCESSION 9977257
 NID
 KEYWORDS EST.
 SOURCE

rat primer-M13 Reverse library-Rat PC-12 cells, untreated
 vector-pBluescript SK- RsaI-EcoRI Rsite2-XhoI poly(A)+ RNA was
 purified from untreated PC12 cells cultured for 9 days. cDNA was
 constructed using an oligo-dT primer and directionally cloned using
 the Lambda ZAP II Vector Kit by Stratagene.
 Rattus sp.

ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;
 Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 279)

AUTHORS Lee,N.H., Weinstock,K.G., Kirkness,E.F., Earle-Hughes,J.A.,
 Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D.,
 Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
 TITLE Comparative expressed sequence tag analysis of differential gene
 expression profiles in PC-12 cells before and after nerve growth
 factor treatment

JOURNAL Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)
 COMMENT Other ESTs: EST106322

CONTACT: Lee NH

The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423

Email: nhlee@tigr.org

For clone availability please contact the TIGR Database

(tdbinfo@db.tigr.org).

FEATURES

source
 Location/Qualifiers
 1..279
 /organism="Rattus sp."

RESULT	12
LOCUS	HSC3LC012 337 bp RNA EST 21-SEP-1995
DEFINITION	H. sapiens partial cDNA sequence; clone c-3lc01.
ACCESSION	F10881
NID	9709398
KEYWORDS	partial cDNA sequence; transcribed sequence fragment.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarhini; Hominidae; Homo. 1 (bases 1 to 337)
AUTHORS	Genexpress.
TITLE	Direct Submission
JOURNAL	Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France. E-mail: genexpress@genethon.fr
REFERENCE	2 (bases 1 to 337)
AUTHORS	Genexpress.
TITLE	The Genexpress cDNA program
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 337)
AUTHORS	Auffray C., Behar G., Bois F., Bouchier C., da Silva C., Devignes M.D., Duprat S., Houlgatte R., Jumeau M.N., Lamy B., Lorenzo F., Mitchell H., Mariage-Samson R., Pietu G., Pouliot Y., Sebastiani-Kabaktchis C. and Tessier A.
TITLE	IMAGS: molecular integration of the analysis of the human genome and its expression
JOURNAL	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE	95277534
COMMENT	Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector; Sequencing_method: single read, full automatic; Primer: (-21)M13 universal; cDNA sequence complementary to mRNA (3'end) Stretch_removed: removed at sequence 5'end Normalization_method: Bento Soares, P.N.A.S. 91:9228-9232(1994); Genexpress_library_idt: C; Genexpress_sequence_idt: alc-3lc01.
FEATURES	source
	1..337
	/organism="Homo sapiens"
	/isolate="muscular atrophy patient"
	/clone_lib="normalized infant brain cDNA from B.Soares, Psychiatry Dept. Columbia University USA"
	/sex="female"
	/tissue_type="total brain"
	/dev_stage="3 months old"
BASE COUNT	101 a 78 c 92 g 64 t 2 others
ORIGIN	
	Query Match 1.98; Score 24; DB 109; Length 337;
	Best Local Similarity 69.4%; Pred.No. 4.59e-05;
	Matches 43; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Db	266 ggaaacatctcggttggttcggaagtaaatgcattcaaacaggagaacaggagat 325
Cp	649 GGAAACCTCTCTGTGTCCTGGGCTACCTGCTCCTCAGAAGCAGAGCGGCAGGCT 590
Db	326 ct 327
Cp	589 CT 588
RESULT	13
LOCUS	N92010 358 bp mRNA EST 04-APR-1996
DEFINITION	za2ia11.r1 Homo sapiens cDNA clone 293180 5' similar to gb:M10942_cds1 Human metallothionein-Ie gene (HUMAN);.
ACCESSION	N92010
NID	91264319
KEYWORDS	EST.
SOURCE	human clone=293180 primer=mob.REGA+ET library=Soares fetal liver

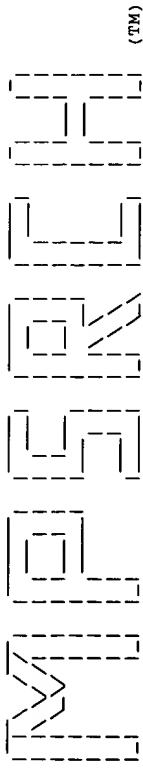
adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pV73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19." NbHL19.

```

NBHH19W:
/clone="356867"
/clone_lib="Soares fetal heart NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"

```

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***** (TM) *****

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Aug 21 14:00:02 1997; MasPar time 343.89 Seconds
Tabular output not generated.
1028.472 Million cell updates/sec

Title: >US-08-320-157-8
Description: (1-1287) from US08320157.seq
Perfect Score: 1287
N.A. Sequence: 1 TTTTATATATAAATTAATGTC.....CCTCAGAGTACAGAGCTT 1287
Comp: AANAATTATATTAATTAACAC.....GGAGTTCATGCTTCGAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 359085 seqs, 137405154 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:
EST-STS-THREE
1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204
7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210
13:EST211 14:EST212 15:EST213 16:EST214 17:EST215
18:EST216 19:EST217 20:EST218 21:EST219 22:EST220
23:EST221 24:EST222 25:EST223 26:EST224 27:EST225
28:EST226 29:EST227 30:EST228 31:EST229 32:EST230
33:EST231 34:EST232 35:EST233 36:STS1 37:STS2 38:STS3
39:STS4 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
46:STS11 47:STS12 48:STS13

EST-STS-FOUR
49:gnEST1 50:gnEST2 51:gnEST3 52:gnEST4 53:gnEST5
54:gnEST6 55:gnEST7 56:gnEST8 57:gnEST9 58:gnEST10
59:gnEST11 60:gnEST12 61:gnEST13 62:gnEST14 63:gnEST15
64:gnEST16 65:gnEST17 66:gnEST18 67:gnEST19 68:gnEST20
69:gnEST21 70:gnEST22 71:gnEST23 72:gnEST24 73:gnEST25
74:gnEST5 75:gnEST1 76:gnEST2 77:gnEST3 78:gnEST4
79:gnEST8 80:gnEST6 81:gnEST7 82:gnEST8 83:gnEST9
84:gnEST10 85:gnEST11 86:gnEST12 87:gnEST13 88:gnEST14
89:gnEST15 90:gnEST16 91:gnEST17 92:gnEST18 93:gnEST19
94:gnEST20 95:gnEST21 96:gnEST22 97:gnEST23 98:gnEST24
99:gnEST25 100:gnEST26 101:gnEST27 102:gnEST28
103:gnEST29 104:gnEST30 105:gnEST31 106:gnESTs 107:ueEST1
108:ueEST2

Database:
49:gnEST1 50:gnEST2 51:gnEST3 52:gnEST4 53:gnEST5
54:gnEST6 55:gnEST7 56:gnEST8 57:gnEST9 58:gnEST10
59:gnEST11 60:gnEST12 61:gnEST13 62:gnEST14 63:gnEST15
64:gnEST16 65:gnEST17 66:gnEST18 67:gnEST19 68:gnEST20
69:gnEST21 70:gnEST22 71:gnEST23 72:gnEST24 73:gnEST25
74:gnEST5 75:gnEST1 76:gnEST2 77:gnEST3 78:gnEST4
79:gnEST8 80:gnEST6 81:gnEST7 82:gnEST8 83:gnEST9
84:gnEST10 85:gnEST11 86:gnEST12 87:gnEST13 88:gnEST14
89:gnEST15 90:gnEST16 91:gnEST17 92:gnEST18 93:gnEST19
94:gnEST20 95:gnEST21 96:gnEST22 97:gnEST23 98:gnEST24
99:gnEST25 100:gnEST26 101:gnEST27 102:gnEST28
103:gnEST29 104:gnEST30 105:gnEST31 106:gnESTs 107:ueEST1
108:ueEST2

Statistics: Mean 11.601; Variance 2.220; scale 5.227

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	94	7.3	1258	38	G06794	human STS WI-7983.	5.87e-129
2	55	4.3	133	91	MM1142620	mt62a08.r1 Soares 2Nb	2.88e-54
3	55	4.3	133	61	AA185611	mt62a08.r1 Soares 2Nb	2.88e-54
4	55	4.3	133	13	AA185611	mt62a08.r1 Soares 2Nb	2.88e-54
5	40	3.1	310	7	AA123834	mp93c04.r1 Soares 2Nb	2.02e-28
6	40	3.1	310	98	MMAA23834	mp93c04.r1 Soares 2Nb	2.02e-28
7	40	3.1	310	58	AA123834	mp93c04.r1 Soares 2Nb	2.02e-28
8	39	3.0	320	56	AA139013	mr04a06.r1 Soares mou	8.38e-27
9	39	3.0	331	49	AA220617	my25f11.r1 Barstead m	8.38e-27
10	39	3.0	331	108	MM1139075	mv25f11.r1 Barstead m	8.38e-27
c 11	26	2.0	475	104	MMAA84020	mt22d08.r1 Soares mou	1.07e-07
c 12	26	2.0	475	59	AA184020	mt22d08.r1 Soares mou	1.07e-07
c 13	26	2.0	475	13	AA184020	mt22d08.r1 Soares mou	1.07e-07
c 14	24	1.9	228	1	N98063	2149C3 czappPFD2.1, D	3.33e-05
15	25	1.9	289	1	N98077	2232C3 czappPFD2.1, D	1.98e-06
c 16	24	1.9	318	17	AA198152	mw49a10.r1 Soares mou	3.33e-05
c 17	24	1.9	412	25	N59408	yv5le02.sl Soares fet	3.33e-05
c 18	24	1.9	442	8	AA126907	z187b04.sl Stratagene	3.33e-05
19	24	1.9	457	15	AA191208	zq45f01.r1 Stratagene	3.33e-05
20	24	1.9	553	4	AA115608	zk89a06.r1 Soares pre	3.33e-05
c 21	24	1.9	560	4	AA115474	zk89a06.sl Soares pre	3.33e-05
c 22	23	1.8	99	25	N58693	yv64f10.r1 Soares fet	5.10e-04
c 23	23	1.8	250	40	G14786	human STS SHGC-13548.	5.10e-04
c 24	23	1.8	283	1	N97744	l186C3 czappPFD2.1, D	5.10e-04
25	23	1.8	301	56	AA138853	mr03a06.r1 Soares mou	5.10e-04
26	23	1.8	311	104	MMAA89753	mt97c07.r1 Soares mou	5.10e-04
27	23	1.8	311	59	AA189753	mt97c07.r1 Soares mou	5.10e-04
28	23	1.8	311	15	AA189753	mt97c07.r1 Soares mou	5.10e-04
29	23	1.8	320	64	AA231246	mw38h09.r1 Soares mou	5.10e-04
30	23	1.8	320	99	MMAA31246	mw38h09.r1 Soares mou	5.10e-04
31	23	1.8	327	24	HUMSUPY306	Human brain cDNA (fet	5.10e-04
32	23	1.8	344	9	AA130593	zol2h07.sl Stratagene	5.10e-04
c 33	23	1.8	372	40	G14445	human STS SHGC-10121.	5.10e-04
c 34	23	1.8	385	93	MM1171296	mz84f08.r1 Soares mou	5.10e-04
35	23	1.8	385	72	AA254866	mz84f08.r1 Soares mou	5.10e-04
36	23	1.8	395	1	N97957	l1718C3 czappPFD2.1, D	5.10e-04
c 37	23	1.8	465	42	G21837	human STS WI-11990.	5.10e-04
38	23	1.8	474	62	CPAA24645	CpEST.117 psKlIminusC	5.10e-04
39	23	1.8	474	80	CPAA24645	CpEST.117 psKlIminusC	5.10e-04
c 40	23	1.8	492	6	AA121520	zk88g10.sl Soares pre	5.10e-04
41	22	1.7	286	12	AA182287	mt76h12.r1 Soares mou	6.99e-03
42	22	1.7	297	79	BM4163	RRAMCA1275SK Bruglia m	6.99e-03
c 43	22	1.7	349	17	AA197101	zq10f12.r1 Stratagene	6.99e-03
44	22	1.7	364	71	AA250729	zr77f05.r1 Soares NhH	6.99e-03
c 45	22	1.7	534	104	MMAA85558	mt62e08.r1 Soares 2Nb	6.99e-03

ALIGNMENTS

1
RESULT LOCUS
G06794 human STS WI-7983.
DEFINITION
Accession
NID
G06794
8660039
KEYWORDS
STS sequence; primer; sequence tagged site.
SOURCE
human STSs derived from sequences in dbEST and the Unigene
Collection.
ORGANISM
Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 1258)
Hudson, T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research

9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: CTGATAACTTGGGAGGCAA
Primer B: GAGAGTCCAACTGCARAGGC
SVS size: 345
PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 nM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from U16811 -- Unigene.

```

FEATURES
  source          Location/Qualifiers
    Sfs           1..1258
                  /organism="Homo sapiens"
                  /map="751_A_7; 787_E_4; 908_C_6; 923_D_2; 919_D_10;
                  942_A_12; 808_G_(6,11)"
    primer_bind   281..300
                  /map="751_A_7; 787_E_4; 908_C_6; 923_D_2; 919_D_10;
                  942_A_12; 808_G_(6,11)"
    primer_bind   complement(606..625)
                  /map="751_A_7; 787_E_4; 908_C_6; 923_D_2; 919_D_10;
                  942_A_12; 808_G_(6,11)"
  BASE COUNT    236 a 356 c 355 g 301 t 10 others
  ORIGIN

Query Match      7.3%; Score 94; DB 38; Length 1258;
Best Local Similarity 95.4%; Pred. No. 5,87e-129;
Matches 104; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1 ctcccaagggtgccccttgggtcccggttcagaccctgcctggacttaagcgaagtctt 60
QY 1180 CTCCTCAAGGTGCCTTTGGGTCCCGTTCAGACCCCTGCTGACCTTAAGCGAAGTCTT 1239

Db 61 tgccttcctgtcccttcgaggggtccccctcgaaggtacagaagctt 109
QY 1240 TGCCTTCTCTGCTCC-CTTCAGGGTCCCGCTCAAGAGTACAGAAGCTT 1287

RESULT 2
ID MM1142620 standard; RNA; EST; 133 BP.
AC AA185611;
NI 91769266
DT 21-FEB-1997 (Rel. 51, Created)
DE mt62a08.r1 Soares 2NbMT Mus musculus cDNA clone 634454 5' similar
DE to TR:G595926 G595926 BAK-2 PROTEIN. ;
KW EST.
OS Mus musculus (house mouse)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-133
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,

```

```

RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RA "The WashU-HHMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
CC Washington University School of MedicineP 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through LLNL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:386446 Trace
CC considered overall poor quality Possible reversed clone: similarity
CC on wrong strand Seq primer: -28M13 rev2 from Amersham High quality
CC sequence strand 1.
FH Key Location/Qualifiers
FH 1..133
FT source
FT /organism="Mus musculus"
FT /strain="C57BL/6J"
FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FT was primed with a Not I - oligo(dT) primer [5'
FT TGTACCAATCTGAAGTGGGAGCGCCGCTTTTCTTTTCTTTTCTTTTCTTTT
FT 3']; double-stranded cDNA was ligated to Eco RI adaptors
FT (Pharmacia), digested with Not I and cloned into the Not I
FT and Eco RI sites of the modified pT7T3 vector. RNA provide
FT by Dr. Bertrand Jordan. Library went through two rounds of
FT normalization, and was constructed by Bento Soares and
FT M.Fatima Bonaldo."
FT /clone_lib="Soares 2NbMT"
FT /sex="male"
FT /tissue_type="Thymus"
FT /dev_stage="4 weeks"
FT /lab_host="DH10B"
FT <1..>133
SQ Sequence 133 BP; 33 A; 40 C; 34 G; 26 T; 0 other;

Query Match      4.3%; Score 55; DB 91; Length 133;
Best Local Similarity 81.6%; Pred. No. 2.88e-54;
Matches 71; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 41 ccgtccctcttgacagcaggtgcccagtcagacagcagcaggtcttccgaagctgta 100
QY 601 CCCCTCTCTTCTTGGAGGAGGTAGCCCGACAGCAGGAGGTTTCCGAGCTACGTT 660

Db 101 tttaccttcaccagcaggaacatgag 127
QY 661 TTTTACCACCATCAGCAGGACAGGAG 687

RESULT 3
LOCUS AA185611 133 bp mRNA EST 19-FEB-1997
DEFINITION mt62a08.r1 Soares 2NbMT Mus musculus cDNA clone 634454 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;
ACCESSION AA185611
NID 91769266
SOURCE EST.
ORGANISM house mouse.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 133)
AUTHORS Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
Waterston R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)

```

COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:386446

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 1.

FEATURES

source

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1..133
/organism="Mus musculus"
/strain="C57BL/6J"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAGAGCGGCGCGGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
/clone="634454"
/clone_lib="Soares 2NbMT"
/sex="male"
/dev_stage="4 weeks"
/tissue_type="Thymus"
/lab_host="DH10B"
<1..>133

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BASE COUNT      33 a  40 c  34 g  26 t
ORIGIN

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Query Match      4.3%; Score 55; DB 61; Length 133;
Best Local Similarity 81.6%; Pred. No. 2.88e-54;
Matches 71; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db 41 ccgtccctcttgacagcaggttgcccatgacacagcagcaggtcttcgaagctacgta 100
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 CCCTCTCTCTGTGAGGACGAGTGTAGCCAGCAGCAGCAGGAGGTTTCCGCGAGCTACGTT 660
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 ttctacctcaccagcaggaacatgag 127
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 TTTTACCACCATCAGCAGGAACAGGAG 687
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 4
LOCUS      AA185611      133 bp      mRNA      EST      07-JAN-1997
DEFINITION mt62a08.r1 Soares 2NbMT Mus musculus cDNA clone 634454 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;

```

```

ACCESSION  AA185611
NID         gl769266
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus

```

```

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

```

REFERENCE

AUTHORS

1 (bases 1 to 133)
 Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE

JOURNAL

COMMENT

The WashU-HHMI Mouse EST Project
 Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:386446

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 1.

FEATURES

source

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1..133
/organism="Mus musculus"
/strain="C57BL/6J"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; [5'
TGTACCAATCTGAGAGCGGCGGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
/clone="634454"
/clone_lib="Soares 2NbMT"
/sex="male"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>133

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BASE COUNT      33 a  40 c  34 g  26 t
ORIGIN

```

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Query Match      4.3%; Score 55; DB 13; Length 133;
Best Local Similarity 81.6%; Pred. No. 2.88e-54;
Matches 71; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db 41 ccgtccctcttgacagcaggttgcccatgacacagcagcaggtcttcgaagctacgta 100
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 CCCTCTCTCTGTGAGGACGAGTGTAGCCAGCAGCAGGAGGTTTCCGCGAGCTACGTT 660
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 101 ttctacctcaccagcaggaacatgag 127
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 661 TTTTACCACCATCAGCAGGAACAGGAG 687
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 5
LOCUS      AA123834      310 bp      mRNA      EST      21-NOV-1996
DEFINITION mp93c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;

```

```

ACCESSION  AA123834
NID         gl1682242
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus

```

```

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

```

REFERENCE

AUTHORS

1 (bases 1 to 310)
 Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE

JOURNAL

COMMENT

The WashU-HHMI Mouse EST Project
 Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of MedicineP


```

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACGAATCTCAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[GTGATTCGGTAC], digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."
/clone="696909"
/sex="mixed"
/dev_stage="7 day"
/lab_host="DH10B"
<1..>331
BASE COUNT      78 a 104 c 89 g 60 t
ORIGIN

Query Match      3.0%; Score 39; DB 49; Length 331;
Best Local Similarity 84.2%; Pred. No. 8.38e-27;
Matches 48; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 275 ccgctccctctgacagcaggtgtccagacacagcagcaggtcttcgaagctac 331
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 601 CCCTCTGCTCTGAGGACAGGTAGTCCAGGACACAGAGGAGGTTTCCCGCAGCTAC 657

RESULT 10
ID MM1139075 standard; RNA; EST; 331 BP.
AC AA220617;
NI G1838404
DT 13-FEB-1997 (Rel. 50, Created)
DE my25f11.r1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA
KW clone 696909 5'.
OS Mus musculus (house mouse)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-331
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RT "The WashU-HMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project
CC Washington University School of Medicine 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through LNL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:430459 Seq
CC primer: -28m13 rev2 ET from Amersham.
CC Location/Qualifiers
FH 1-331
FH source
FH 1..331
FH /organism="Mus musculus"
FH /strain="FVB/N"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
FH was primed with a Not I - oligo(dT) primer [5',
FH TGTACGAATCTCAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT
FH 3']; double-stranded cDNA was ligated to Eco RI adaptors
FH [GTGATTCGGTAC], digested with Not I and cloned into the
FH Not I and Eco RI sites of the modified pT7T3 vector.
FH Library constructed by Bob Barstead."
FH /clone="696909"
FH /sex="mixed"
FH /dev_stage="7 day"
FH /lab_host="DH10B"
FH 1..331
FH /organism="Mus musculus"
FH /strain="FVB/N"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
FH was primed with a Not I - oligo(dT) primer [5',
FH TGTACGAATCTCAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT
FH 3']; double-stranded cDNA was ligated to Eco RI adaptors
FH [GTGATTCGGTAC], digested with Not I and cloned into the
FH Not I and Eco RI sites of the modified pT7T3 vector.
FH Library constructed by Bob Barstead."
FH /clone="696909"
FH /sex="mixed"
FH /dev_stage="7 day"
FH /lab_host="DH10B"

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FT mRNA
SQ Sequence 331 BP; 78 A; 104 C; 89 G; 60 T; 0 other;

Query Match      3.0%; Score 39; DB 108; Length 331;
Best Local Similarity 84.2%; Pred. No. 8.38e-27;
Matches 48; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 275 ccgctccctctgacagcaggtgtccagacacagcagcaggtcttcgaagctac 331
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 601 CCCTCTGCTCTGAGGACAGGTAGTCCAGGACACAGAGGAGGTTTCCCGCAGCTAC 657

RESULT 11
ID MMA84020 standard; RNA; EST; 475 BP.
AC AA184020;
NI G1767585
DT 19-FEB-1997 (Rel. 51, Created)
DE 19-FEB-1997 (Rel. 51, Last updated, Version 1)
DE mt22d08.r1 Soares mouse 3NbMS Mus musculus cDNA clone 621807 5'.
KW EST.
OS Mus musculus (house mouse)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-475
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RT "The WashU-HMI Mouse EST Project";
RL Unpublished.
CC Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project
CC Washington University School of Medicine 4444 Forest Park Parkway,
CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC Email: mouseest@wustl.edu This clone is available
CC royalty-free through LNL; contact the IMAGE Consortium
CC (info@image.llnl.gov) for further information. MGI:382631 Seq
CC primer: -28M13 rev2 from Amersham High quality sequence stop: 438.
CC Location/Qualifiers
FH 1..475
FH source
FH 1..475
FH /organism="Mus musculus"
FH /strain="C57BL/6J"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FH was primed with a Not I - oligo(dT) primer [5',
FH TGTACGAATCTCAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT
FH 3']; double-stranded cDNA was ligated to Eco RI adaptors
FH (Pharmacia), digested with Not I and cloned into the Not I
FH and Eco RI sites of the modified pT7T3 vector. RNA provide
FH by Dr. Bertrand Jordan. Library went through three rounds
FH of normalization, and was constructed by Bento Soares and
FH M.Fatima Bonaldo."
FH /clone_lib="Soares mouse 3NbMS"
FH /clone="621807"
FH /sex="male"
FH /tissue_type="Spleen"
FH /dev_stage="4 weeks"
FH /lab_host="DH10B"
FH 1..>475
FH mRNA
SQ Sequence 475 BP; 150 A; 56 C; 67 G; 202 T; 0 other;

Query Match      2.0%; Score 26; DB 104; Length 475;
Best Local Similarity 76.0%; Pred. No. 1.07e-07;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 291 ttctaataatttcatttcgtataacatttaaacatttcctttgagtaattt 340
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Cp 94 TTTTCATCTTTTTCAGTCTCTATACATTTTGAATTTTATTAAATATTATTT 45

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RESULT	12										
LOCUS	AA184020	475 bp	mRNA	EST	17-FEB-1997						
DEFINITION	mt22408.r1 Soares mouse 3NbMS Mus musculus cDNA clone 621807 5'.										
ACCESSION	AA184020										
NID	g1767585										
KEYWORDS	EST.										
SOURCE	house mouse.										
ORGANISM	Mus musculus										
REFERENCE	1 (bases 1 to 475)										
AUTHORS	Karrar,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisei,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.										
TITLE	The WashU-HMI Mouse EST Project										
JOURNAL	Unpublished (1996)										
COMMENT	Contact: Maira M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:382631 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 438. Location/Qualifiers 1..475 /organism="Mus musculus" /strain="C57BL/6J" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAACTGAAGTGGAGCGCGCGCTGTGTGTGTGTGTGTGTGTGT 3'] ; Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector' RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo." /clone="621807" /clone_lib="Soares mouse 3NbMS" /sex="male" /tissue_type="Spleen" /dev_stage="4 weeks" /lab_host="DH10B" <1..>475										
BASE COUNT	150 a	56 c	67 g	202 t							
ORIGIN											
Query Match	2.0%	Score 26;	DB 59;	Length 475;							
Best Local Similarity	76.0%;	Pred. NO. 1.07e-07;									
Matches	38;	Conservative	0;	Mismatches 12;	Indels	0;	Gaps	0;			
Db	291	tctcaatatttctcatcttctgaacatttaaccttccttgagtaattt 340									
Cp	94	TTTTCACTTTTTCAGTCTCTATACATTTGAATTTTATTAAGTATATT 45									
RESULT	13										
LOCUS	AA184020	475 bp	mRNA	EST	07-JAN-1997						
DEFINITION	mt22408.r1 Soares mouse 3NbMS Mus musculus cDNA clone 621807 5'.										
ACCESSION	AA184020										
NID	g1767585										
KEYWORDS	EST.										
SOURCE	house mouse.										

Search completed: Thu Aug 21 14:17:25 1997
Job time : 1043 secs.

Search completed: Thu Aug 21 14:17:25 1997
Job time : 1043 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

```

mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on:      Wed Aug 20 11:04:54 1997;  Maspar time 5.42 Seconds
              445.465 Million cell updates/sec
Tabular output not generated.

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>US-08-320-157-9
Title:
Description: (1-211) from US08320157.pep
Perfect Score: 1554
Sequence: 1 MASGGGPPPPRQCEGEPALP .....LWLGVLLGQFVYRREFFKS 211
```

Scoring table: PAM 150
Gap 11

Searched: 96640 seqs, 11439865 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq27

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20

Statistics: Mean 32.557; Variance 141.390; scale 0.230

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
1	1554	100.0	211	20	W03659	Bak-2 protein.	8.16e-138	
2	1554	100.0	211	13	R77877	Human Cdn-2.	8.16e-138	
3	1529	98.4	211	13	R77876	Human Cdn-1.	2.32e-135	
4	1529	98.4	211	20	W03658	Bak protein.	2.32e-135	
5	1529	98.4	211	17	R81451	Bcl-y apoptosis-relat	2.32e-135	
6	1136	73.1	152	13	R77879	Human Cdn-1(60-211).	6.78e-97	
7	1061	68.3	141	13	R77880	Human Cdn-1(71-211).	1.38e-89	
8	880	56.6	116	13	R77881	Human Cdn-1(96-211).	5.18e-72	
9	275	17.7	232	19	W01020	Apoptosis-blocking pr	9.24e-15	
10	271	17.4	190	13	R68884	Chicken lymphoid BCL-	2.11e-14	
11	264	17.0	233	13	R68887	Human thymus BCL-XL.	8.96e-14	
12	264	17.0	233	20	W05821	Bcl-XL protein.	8.96e-14	
13	262	16.9	232	19	W01019	Apoptosis-blocking pr	1.35e-13	
14	262	16.9	239	19	W01018	Apoptosis-blocking pr	1.35e-13	
15	260	16.7	205	13	R71405	Human bcl-2 beta prot	2.04e-13	
16	260	16.7	205	13	R68886	Human thymus BCL-2.	2.04e-13	
17	260	16.7	205	13	R70332	Human bcl-2 protein.	2.04e-13	
18	260	16.7	239	13	R71404	Human bcl-2 alpha pro	2.04e-13	
19	260	16.7	239	9	R47387	Human oncogene bcl-2	2.04e-13	
20	260	16.7	239	1	P80387	Sequence of bcl-2-alp	2.04e-13	

Db 61 vtllpqsstmgvgrqlaigddlnrrydsfqtmlqlhqlptaenayeyftkiasslife 120
 QY 61 vtllpqsstmgvgrqlaigddlnrrydsfqtmlqlhqlptaenayeyftkiasslife 120
 Db 121 sginwrvallgfsrlyalhlyqrgltfqlgqtrfvvdfmlhcliarwiagrgwvaa 180
 QY 121 sginwrvallgfsrlyalhlyqrgltfqlgqtrfvvdfmlhcliarwiagrgwvaa 180
 Db 181 lnlgngpilnlvlgvllgfvvrrffks 211
 QY 181 lnlgngpilnlvlgvllgfvvrrffks 211

RESULT 2

ID R77877 standard; Protein; 211 AA.
 AC R77877;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-2.
 KW Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN WO9515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; US-160067.
 PR 30-NOV-1994; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 95-215106/28;
 DR N-PSDB: Q95493.
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure: Fig. 5D-E; 6pp; English.
 CC Cdn-2 cDNA was isolated from a human placental genomic library
 CC using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
 CC in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced
 CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
 CC with Cdn-1 (R77875).
 SQ Sequence 211 AA;

Query Match 100.0%; Score 1554; DB 13; Length 211;
 Best Local Similarity 100.0%; Pred. No. 8.16e-138;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 masggpgpprgecgepalpsaseeqvaqdtteevfsvfyrhqqeagaaapadpem 60
 QY 1 MASGGPGPPRGECEGEPALPSASEEQVAQDTEEVFSVYFHHQQEAGAAAPADPEM 60
 Db 61 vtllpqsstmgvgrqlaigddlnrrydsfqtmlqlhqlptaenayeyftkiasslife 120
 QY 61 vtllpqsstmgvgrqlaigddlnrrydsfqtmlqlhqlptaenayeyftkiasslife 120
 Db 121 sginwrvallgfsrlyalhlyqrgltfqlgqtrfvvdfmlhcliarwiagrgwvaa 180
 QY 121 sginwrvallgfsrlyalhlyqrgltfqlgqtrfvvdfmlhcliarwiagrgwvaa 180
 Db 181 lnlgngpilnlvlgvllgfvvrrffks 211
 QY 181 lnlgngpilnlvlgvllgfvvrrffks 211

RESULT 3

ID R77876 standard; Protein; 211 AA.
 AC R77876;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-1.
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.

PN WO9515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; US-160067.
 PR 30-NOV-1994; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 95-215106/28;
 DR N-PSDB: Q95492.
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure: Fig. 3A-B; 6pp; English.
 CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
 CC previously isolated clone as probe. Recombinant Cdn-1 was produced
 CC in Sf9 and human colon adenocarcinoma Hc29 cells. Expression of
 CC Cdn-1 in WI-12 lymphoblastoid cells resulted in increased cell
 CC survival in response to anti-fas-mediated apoptosis.
 SQ Sequence 211 AA;

Query Match 98.4%; Score 1529; DB 13; Length 211;
 Best Local Similarity 97.2%; Pred. No. 2.32e-135;
 Matches 205; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Db 1 masggpgpprgecgepalpsaseeqvaqdtteevfsvfyrhqqeagaaapadpem 60
 QY 1 MASGGPGPPRGECEGEPALPSASEEQVAQDTEEVFSVYFHHQQEAGAAAPADPEM 60
 Db 61 vtllpqsstmgvgrqlaigddlnrrydsfqtmlqlhqlptaenayeyftkiasslife 120
 QY 61 vtllpqsstmgvgrqlaigddlnrrydsfqtmlqlhqlptaenayeyftkiasslife 120
 Db 121 sginwrvallgfsrlyalhlyqrgltfqlgqtrfvvdfmlhcliarwiagrgwvaa 180
 QY 121 sginwrvallgfsrlyalhlyqrgltfqlgqtrfvvdfmlhcliarwiagrgwvaa 180
 Db 181 lnlgngpilnlvlgvllgfvvrrffks 211
 QY 181 lnlgngpilnlvlgvllgfvvrrffks 211

RESULT 4

ID WO3668 standard; Protein; 211 AA.
 AC WO3668;
 DT 22-FEB-1997 (first entry)
 DE Bak protein.
 KW Human; Bak; apoptosis; latency; virus replication;
 KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.
 OS Homo sapiens.
 PN WO9633416-A1.
 PD 24-OCT-1996.
 PF 19-APR-1996; US5639.
 PR 20-APR-1995; US-462529.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 96-485886/48.
 DR N-PSDB: T42138.
 PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 PS Disclosure: Fig 1; 24pp; English.
 CC This Bak protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
 CC protein, and is capable of modulating apoptosis. The protein may
 CC be used in complete or partial form, or as an epitope tag fusion
 CC protein, in a new virucide drug screening method, which involves
 CC combination of Bak protein and a viral protein (e.g. EBV BHRF1),
 CC exposure to a test compound, and monitoring for disruption of the
 CC interaction, e.g. by co-precipitation, protein interactive trapping
 CC or ELISA. Interaction of Bak and viral proteins allows viral

CC replication or latency in the absence of apoptosis. Compounds which
 CC inhibit the interaction may be used as virucide, antitumour or
 CC diagnostic agents.
 SQ Sequence 211 AA;

Query Match 98.4%; Score 1529; DB 20; Length 211;
 Best Local Similarity 97.2%; Pred. No. 2,32e-135;
 Matches 205; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 masqgppprqecgepalpsaseeqvaqdtveefrsvfyrhqegeaegvaapadpem 60
 QY 1 MASQGGPPPRQECGEPALPSASEEQVAQDTVEEFRSVFYRHQEQEAEAGAAAPADPEM 60

Db 61 vtlpqpssstmgqgrqlaigddinrydsefqtmlqlhqlptaenayeyftkiatslfe 120
 QY 61 VTLPQPSSSTMGQGRQLAIGDDINRYDSEFQTMQLHQLPTAENAYEYFTKIASSLFE 120

Db 121 sginwgrvvalgfgyrlalhvlyghgtgflgqvtrfvvdfmlhbciaarwiaqrggwaa 180
 QY 121 SGINWGRVVALGFSYRLALHVIYQGLTGFLGQVTRFVDFMLHHCIAARWIAQRGGWAA 180

Db 181 lnlgngpnlvvlvgvllgqfvrrffks 211
 QY 181 LNLGNGPILNLVVLVGVLLGQFVVRFFKS 211

RESULT 5
 ID R81451 standard; Protein; 211 AA.
 AC R81451;
 DT 02-JUL-1996 (first entry)
 DE Bcl-Y apoptosis-related protein.
 KW Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis;
 KW therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 188..205
 FT /label= C-terminal domain
 FT /note= "putative membrane localisation sequence"
 PN W09605232-A1.
 PD 22-FEB-1996.
 PF 09-AUG-1995; U10103.
 PR 09-AUG-1994; US-287427.
 PR 11-OCT-1994; US-321071.
 PA (IMMUNO) IMMUNOGEN INC.
 PI Chittenden ID;
 DR WPI; 96-139648/14.
 DR N-PSDB; T17375.

PT New isolated human Bcl-Y protein - used to develop prods. for
 PT treating disorders characterised by inappropriate cell proliferation
 PT or cell death
 PS Claim 3; Fig 4; 100pp; English.

CC Bcl-Y protein (R81451) is a member of the Bcl-2 family and can
 CC induce apoptosis in cells and function as a negative regulator of
 CC Bcl-2 function. Bcl-Y mRNA was detected in all human tumour cell
 CC lines examined and is also widely expressed in primary human
 CC tissues. It can be obt'd. by expression of a full-length cDNA
 CC clone (T17375) in pref. mammalian host cells. Bcl-Y can be used to
 CC develop prods. for treating disorders associated with inappropriate
 CC cell proliferation or cell death, and to raise antibodies used for
 CC the diagnosis or monitoring of such disorders.
 SQ Sequence 211 AA;

Query Match 98.4%; Score 1529; DB 17; Length 211;
 Best Local Similarity 97.2%; Pred. No. 2,32e-135;
 Matches 205; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 masqgppprqecgepalpsaseeqvaqdtveefrsvfyrhqegeaegvaapadpem 60
 QY 1 MASQGGPPPRQECGEPALPSASEEQVAQDTVEEFRSVFYRHQEQEAEAGAAAPADPEM 60

Db 61 vtlpqpssstmgqgrqlaigddinrydsefqtmlqlhqlptaenayeyftkiatslfe 120
 QY 61 VTLPQPSSSTMGQGRQLAIGDDINRYDSEFQTMQLHQLPTAENAYEYFTKIASSLFE 120

Db 121 sginwgrvvalgfgyrlalhvlyghgtgflgqvtrfvvdfmlhbciaarwiaqrggwaa 180
 QY 121 SGINWGRVVALGFSYRLALHVIYQGLTGFLGQVTRFVDFMLHHCIAARWIAQRGGWAA 180

Db 181 lnlgngpnlvvlvgvllgqfvrrffks 211
 QY 181 LNLGNGPILNLVVLVGVLLGQFVVRFFKS 211

RESULT 6
 ID R77879 standard; Protein; 152 AA.
 AC R77879;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-1(60-211).
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN W09515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI; 95-215106/28.
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure; Fig.11; 66pp; English.
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
 CC decreased this activity, suggesting that small, truncated Cdn-1
 CC molecules may be potent therapeutics.
 SQ Sequence 152 AA;

Query Match 73.1%; Score 1136; DB 13; Length 152;
 Best Local Similarity 97.4%; Pred. No. 6,78e-97;
 Matches 148; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvtlplqpsstmgqgrqlaigddinrydsefqtmlqlhqlptaenayeyftkiatslf 60
 QY 60 MVTLPQPSSSTMGQGRQLAIGDDINRYDSEFQTMQLHQLPTAENAYEYFTKIASSLF 119

Db 61 esginwgrvvalgfgyrlalhvlyghgtgflgqvtrfvvdfmlhbciaarwiaqrggwaa 120
 QY 120 ESGINWGRVVALGFSYRLALHVIYQGLTGFLGQVTRFVDFMLHHCIAARWIAQRGGWAA 179

Db 121 alnlgngpnlvvlvgvllgqfvrrffks 152
 QY 180 ALNLGNGPILNLVVLVGVLLGQFVVRFFKS 211

RESULT 7
 ID R77880 standard; Protein; 141 AA.
 AC R77880;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-1(71-211).
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN W09515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI; 95-215106/28.

PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure; Fig.11; 66pp; English.
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
 CC activity, suggesting that small, truncated Cdn-1 molecules may be
 CC potent therapeutics.
 SQ Sequence 141 AA;

Query Match 68.3%; Score 1061; DB 13; Length 141;
 Best Local Similarity 97.2%; Pred. No. 1.38e-89;
 Matches 137; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 mgvgvrglaigddinrrydesfqlmqlhqlptaenayeyftkiatslfesglnwgrva 60
 QY 71 MGQVGROLAIGDDINRRYDSEFTMLQLHQLPTAENAYEYFTKIATSLFESGINWGRVA 130
 Db 61 llqgyrlalhvyghgtglgqvtrfvdfmlhbciaarqagvwaalnlgngpilm 120
 QY 131 LLGFSYRLALHIYQRLGTGLGQVTRFVDFMLHHCIAARQAGVWAALNLGNGPILN 190
 Db 121 vlvlvgvlllgqvrrffks 141
 QY 191 VLVLVGVLVGQFVVRFFKS 211

RESULT 8
 ID R77881 standard; Protein; 116 AA.
 AC R77881;
 DT 21-NOV-1995 (first entry)
 DE Human Cdn-1(96-211)
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN W09515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Klefer MC;
 DR WPI; 95-215106/28.

PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure; Fig.11; 66pp; English.
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Truncated Cdn-1 derivatives given in R77879-81 were used to
 CC test the effects of deleting the N-terminal sequences of Cdn-1
 CC on this activity.
 SQ Sequence 116 AA;

Query Match 56.6%; Score 880; DB 13; Length 116;
 Best Local Similarity 96.6%; Pred. No. 5.18e-72;
 Matches 112; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 mlqlhqlptaenayeyftkiatslfesglnwgrvallygrylalyhvgqltqlgvt 60
 QY 96 MLQHLQPTAENAYEYFTKIATSLFESGINWGRVALLGFSYRLALHIYQRLGTGLGQVT 155
 Db 61 rfvydfmlhbciaarqagvwaalnlgngpilmvlgvllgqvrrffks 116
 QY 156 RFVDFMLHHCIAARQAGVWAALNLGNGPILNLVLVLVGVLVGQFVVRFFKS 211

RESULT 9
 ID W01020 standard; Protein; 232 AA.

AC W01020;
 DT 18-DEC-1996 (first entry)
 DE Apoptosis-blocking protein Bcl-2 mutant 80-6 (del80-86).
 KW Apoptosis-regulating protein; Bcl-2; oncogene;
 KW adenovirus ElB 19K protein; cell death; cancer; tumour;
 KW immune disorder; diagnosis; therapy; BipiA; Bipi3; Bipi5; Nip1;
 KW Nip2; Nip3.
 OS Synthetic.
 PN EP-733706-A2.
 PD 25-SEP-1996.
 PF 21-MAR-1996; 104542.
 PR 21-MAR-1995; US-408095.
 PA (UYSL-) UNIV ST LOUIS.
 PI Chinnadurai G;
 DR WPI; 96-427055/43.
 PT Nucleic acids encoding apoptosis regulating proteins - useful for
 PT diagnosing and treating immune disorders, malignancies, etc.
 PS Example 8; Page 34-35; 60pp; English.
 CC The 80-6 mutant (W01020) of the bcl-2 oncogene product (W01018)
 CC lacks amino acids 80-86 of the native protein. This and other
 CC Bcl-2 mutants (see also W01019-21) were used in a two hybrid assay
 CC to examine the interactions between Bcl-2 and novel apoptosis-
 CC regulating proteins Nip1, Nip2 and Nip3 (W00997-99). 2 Motifs
 CC (W01003-04) on Bcl-2 were identified that are essential for
 CC interaction with the Nip proteins. These motifs show homology
 CC to motifs (W01005-06) identified on the adenovirus ElB 19K
 CC apoptosis-blocking protein (W01010).
 SQ Sequence 232 AA;

Query Match 17.7%; Score 275; DB 19; Length 232;
 Best Local Similarity 29.7%; Pred. No. 9.24e-15;
 Matches 47; Conservative 41; Mismatches 62; Indels 8; Gaps 6;
 Db 48 ffsqsgqthpbaar-dpvartsplqtapaagspyppvvhltlrgagddfsrryrdfa 106
 QY 40 FYHQEQEAEAGAAPADPEMTPLQPSSTMG-QVGR--QLAI--IGDDINRRYDSEFQ 94
 Db 107 emssqhltpftargcfatveelfrdgynvgrivaffegvgmcsvnsplvdni 166
 QY 95 TMLQHLQPTAENAYEYFTKIATSLFESGINWGRVALLGFSYRLALHIYQRLGTGLGQV 154
 Db 167 alwmtelylnrh-lhtwiqnggdwafvel-yqpsmrpl 202
 QY 155 TRFVDFMLHHCIAARQAGVWAALNLGNGPILNLVL 192

RESULT 10
 ID R6884 standard; Protein; 190 AA.
 AC R6884;
 DT 10-AUG-1995 (first entry)
 DE Chicken lymphoid BCL-X.
 KW Chicken; bird; fowl; BCL-X; apoptosis; cell death; cancer;
 KW neurodegenerative disease; autoimmune disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; multiple sclerosis; oncogene.
 OS Gallus domesticus.
 PN W09500642-A.
 PD 05-JAN-1995.
 PF 22-JUN-1994; U07089.
 PR 22-JUN-1993; US-081448.
 PA (ARCH-) ARCH DEV CORP.
 PA (UNMI) UNIV MICHIGAN.
 PI Boise LH, Nunez G, Thompson CB;
 DR WPI; 95-052079/07.
 DR N-PSDB; Q81696.
 PT New poly-nucleotide encoding new poly-peptide(s) that modify
 PT apoptosis - and related vectors, recombinant cells and
 PT antibodies, useful in assay and for control of cell death in e.g.
 PT neuronal cells, lymphocytes and cancers
 PS Claim 4; Page 87; 127pp; English.
 CC This protein may be expressed recombinantly, particularly with pcmv
 CC plasmids as vectors for expression in mammalian cell cultures.
 CC The protein has particular application in cancer cells (failure of
 CC programmed cell death (PCD)) or neurodegenerative and autoimmune diseases

QY 113 KIASLFESGINWGRVVALLGFSYRLALHIYORGLTGFLGQVTRFVVDFMLHHCIARWIA 172

Db 191 dnqgwga 198

QY :|||||
173 QRGWVAA 180

Search completed: Wed Aug 20 11:05:16 1997.
Job time : 22 secs.

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723.119 Million cell updates/sec
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Scoring table: PAM 150
Gap 11

Listing first 45 summaries

Database:
swiss_prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query		Length	DB	ID	Description	Pred. No.
	Score	Match					
1	271	17.4	190	1	BCLX_CHICK	APOPTOSIS REGULATOR B	1.55e-29
2	268	17.2	233	1	BCLX_RAT	APOPTOSIS REGULATOR B	5.65e-28
3	286	17.1	233	1	BCLX2_CHICK	APOPTOSIS REGULATOR B	1.34e-28
4	284	17.0	233	1	BCLX_HUMAN	APOPTOSIS REGULATOR B	3.16e-28
5	256	16.5	205	1	BC2B_HUMAN	PROTEIN BCL-2-BETA.	9.72e-27
6	256	16.5	239	1	BC2A_HUMAN	PROTEIN BCL-2-ALPHA.	9.72e-27
7	251	16.2	199	1	BC2B_MOUSE	PROTEIN BCL-2-BETA.	8.18e-26
8	251	16.2	236	1	BC2A_MOUSE	PROTEIN BCL-2-ALPHA.	8.18e-26
9	250	16.1	236	1	BCL2_RAT	PROTEIN BCL-2 ALPHA.	1.25e-25
10	221	14.2	192	1	BAXA_MOUSE	APOPTOSIS REGULATOR B	2.37e-20
11	208	13.4	192	1	BAXA_HUMAN	APOPTOSIS REGULATOR B	4.87e-18
12	203	13.1	218	1	BAXB_HUMAN	APOPTOSIS REGULATOR B	4.87e-18
13	178	11.5	143	1	BAXD_HUMAN	APOPTOSIS REGULATOR B	3.69e-17
14	179	11.5	350	6	MCL1_HUMAN	INDUCED MYELOID LEUKA	7.30e-13
15	173	11.1	172	5	HSAL_MOUSE	HEMOPOIETIC-SPECIFIC	5.01e-13
16	145	9.3	179	3	EAR_ASF64	APOPTOSIS REGULATOR B	5.09e-12
17	142	9.1	179	3	EAR_ASF57	APOPTOSIS REGULATOR B	1.73e-07
18	139	8.9	179	3	EAR_ASF2	APOPTOSIS REGULATOR B	5.05e-07
19	115	7.4	626	5	HTP3_BACSU	APOPTOSIS REGULATOR B	1.46e-06
20	107	6.9	255	2	CX3C_CAAEL	CYTOSOL SHOCK PROTEIN HT	4.77e-03
21	105	6.8	567	5	HTX2_YEAST	CHROMATIN C OXIDASE	5.81e-02
22	105	6.8	576	5	HXT4_YEAST	LOW-AFFINITY GLUCOSE	1.07e-01
23	105	6.8	576	5	HXT5_YEAST	LOW-AFFINITY GLUCOSE	1.07e-01


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RESULT 5
ID BC2B_HUMAN STANDARD; PRT; 205 AA.
AC P10416;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PROTEIN BCL-2-BETA.
GN BCL2
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE: 86259760.
RA TSUJIMOTO Y., CROCE C.M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
[2]
RN RP REVISIONS TO 96 AND 110.
RX MEDLINE: 92375724.
RA EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
RL NUCLEIC ACIDS RES. 20:4187-4192(1992).
[3]
RN RP SUBCELLULAR LOCATION.
RX MEDLINE: 91066924.
RA HOCKENBERRY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
RL NATURE 348:334-336(1990).
CC -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
CC FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
CC OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC -1- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
CC II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
CC T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
CC REGIONS.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC DIFFER AT THEIR C-TERMINAL ENDS.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL: M13995; G179369; ALT_SEQ.
DR PIR: B29409; TVHUB1.
DR PIR: D37332; D37332.
DR MIM: 151430; -.
DR PROSITE: PS01080; BCL2.
KW PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE;
KW MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
SQ SEQUENCE 205 AA; 22311 MW; ED321E5E CRC32;

Query Match 16.5%; Score 256; DB 1; Length 205;
Best Local Similarity 29.7%; Pred. No. 9.72e-27;
Matches 38; Conservative 35; Mismatches 51; Indels 4; Gaps 3;

Db 74 tpaapgaagapalsvppvvhlt--lrqagddfsrryrdfaemssqlhltptargrfa 131
QY 54 APADPEMVTLP-LQPSMTGQVQLAIGDDINRRYDSEFTQMLQLQPTAENAYEYFT 112
Db 132 tvveelfrdgvnqrivaffefggvmcvesvnrmsplvndialwmtelylnrh-lhtwiq 190
QY 113 KIASSLFESGINWGRVALLGFSYRLALHIYQRLGTLGQVTRFVVDFMLHHCIARWIA 172
Db 191 dnggwvga 198
QY 173 QRGGWVAA 180

RESULT 6
ID BC2A_HUMAN STANDARD; PRT; 239 AA.
AC P10415;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

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DE PROTEIN BCL-2-ALPHA.
GN BCL2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE: 86259760.
RA TSUJIMOTO Y., CROCE C.M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
[2]
RN RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE: 92375724.
RA EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
RL NUCLEIC ACIDS RES. 20:4187-4192(1992).
[3]
RN RP SEQUENCE FROM N.A.
RX MEDLINE: 87002488.
RA CLEARY M.L., SMITH S.D., SKLAR J.;
RL CELL 47:19-28(1986).
[4]
RN RP SUBCELLULAR LOCATION.
RX MEDLINE: 91066924.
RA HOCKENBERRY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
RL NATURE 348:334-336(1990).
CC -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
CC FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
CC OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC -1- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
CC II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
CC T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
CC REGIONS.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC DIFFER AT THEIR C-TERMINAL ENDS.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL: M13994; G179367; ALT_SEQ.
DR EMBL: M14745; G179371; -.
DR PIR: A29409; TVHUAL.
DR PIR: A24428; TVHUBC.
DR PIR: C37332; C37332.
DR MIM: 151430; -.
DR PROSITE: PS01080; BCL2.
KW PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE;
KW MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
FT TRANSMEM 212 233
FT CONFLICT 59 59 P -> T (IN REF. 3).
FT CONFLICT 117 117 S -> R (IN REF. 3).
SQ SEQUENCE 239 AA; 26266 MW; 75084B59 CRC32;

Query Match 16.5%; Score 256; DB 1; Length 239;
Best Local Similarity 29.3%; Pred. No. 9.72e-27;
Matches 41; Conservative 37; Mismatches 57; Indels 5; Gaps 4;

Db 74 tpaapgaagapalsvppvvhlt--lrqagddfsrryrdfaemssqlhltptargrfa 131
QY 54 APADPEMVTLP-LQPSMTGQVQLAIGDDINRRYDSEFTQMLQLQPTAENAYEYFT 112
Db 132 tvveelfrdgvnqrivaffefggvmcvesvnrmsplvndialwmtelylnrh-lhtwiq 190
QY 113 KIASSLFESGINWGRVALLGFSYRLALHIYQRLGTLGQVTRFVVDFMLHHCIARWIA 172
Db 191 dnggwadafvel-ygpsmrpl 209
QY 173 QRGGWVAAALNLGNGPILNVL 192

RESULT 7
ID BC2B_MOUSE STANDARD; PRT; 199 AA.

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CC      -!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC      CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC      ALTERNATIVE SPLICING.
CC      -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR      EMBL; L22473; G388166; -.
DR      PIR; A47538; B47538.
DR      MIM; 600040; -.
DR      PROSITE; PS01080; BCL2.
DR      APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
KW      TRANSMEM 172   192   POTENTIAL.
FT      SEQUENCE 192 AA; 21184 MW; B2E6148A CRC32;

Query Match          13.4%; Score 208; DB 1; Length 192;
Best Local Similarity 24.5%; Pred.No. 4.87e-18;
Matches 40; Conservative 45; Mismatches 71; Indels 7; Gaps

Db    32 qdragrmgeapelpdpvpqdgastkkliseclkrigdelgs--nmelqrniaavdtdspr 89
QY    I : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY    47 QEAEGAAPADPEWVTLPLOPSSIMGVGRQLAIIGDDINRRYDSEFQTMLQHLOPTAEN 106

Db    90 e-vff-rvaadmfsdnfnwgrvvalfyfasklvkalctkvpelirtmgwtldf-lre 146
QY    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY    107 AYEFYTKIASSLFESG-INWGRVVALLGSFYRLALHIHQYRGLTGFLQGTVTFVVDMLHH 165

Db    147 rllgwldqqgvgdllyfgtptwtgtvtifvagvltasltiwk 189
QY    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY    166 CIARIWAQRGGVAALNLGNPGPI-LNVLVLGVLLGQVFVRR 207

RESULT 12
ID     BAXD_HUMAN STANDARD; PRT; 218 AA.
AC     Q07814;
DT     01-FEB-1995 (REL. 31, CREATED)
DI     01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DE     01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE     APOPTOSIS REGULATOR BAX, CYTOPLASMIC ISOFORM BETA.
GN     BAX.
OS     HOMO SAPIENS (HUMAN).
OC     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
NC     EUETHERIA; PRIMATES.
RN     [1]
RP     SEQUENCE FROM N.A.
RC     TISSUE-B-CELL;
RX     MEDLINE; 93364978.
RA     OLTAI Z.N., MILLMAN C.L., KORSMEYER S.J.;
RL     CELL 74:609-619(1993).
CC      -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC      APOPTOSIS REPRESSOR BCL-2.
CC      -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC      -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC      -!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC      CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC      ALTERNATIVE SPLICING.
CC      -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR      EMBL; L22474; G388168; -.
DR      PIR; B47538; B47538.
DR      MIM; 600040; -.
DR      PROSITE; PS01080; BCL2.
DR      APOPTOSIS; ALTERNATIVE SPLICING.
KW      TRANSMEM 218 AA; 24220 MW; 82B2FF09 CRC32;

Query Match          13.1%; Score 203; DB 1; Length 218;
Best Local Similarity 27.0%; Pred No. 3.69e-17;
Matches 37; Conservative 36; Mismatches 58; Indels 6; Gaps

Db    32 qdragrmgeapelpdpvpqdgastkkliseclkrigdelgs--nmelqrniaavdtdspr 89
QY    I : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY    47 QEAEGAAPADPEWVTLPLOPSSIMGVGRQLAIIGDDINRRYDSEFQTMLQHLOPTAEN 106

Db    90 e-vff-rvaadmfsdnfnwgrvvalfyfasklvkalctkvpelirtmgwtldf-lre 146
QY    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY    107 AYEFYTKIASSLFESG-INWGRVVALLGSFYRLALHIHQYRGLTGFLQGTVTFVVDMLHH 165

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QY 166 C1ARWIAQRGGVVAALNLGNGLPIINVL 192

RESULT 10
ID BAXA_MOUSE STANDARD; PRT; 192 AA.
AC QO7813;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN BAX.
GS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; RODENTIA.

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6 X DBA/2 FL;
RX MEDLINE; 93364978.
RL OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
LA CELL 74:609-619(1993).

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

DR EMBL; L22472; G388192; --
DR PROSITE; PS01080; BCL2
KW APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21394 MW; BD035304 CRC32;

Query Match 14.2% Score 221; DB 1; Length 192;
Best Local Similarity 25.6%; Pred.No.2.37e+20;
Matches 46; Conservative 50; Mismatches 75; Indels 9; Gaps

Db 16 seqmktgafllgfqdragmagetpeitlqpqqdstk-klseccrrigdeids-- 72
 :||:::||::||::||::||::||::||::||::||:
QY 31 TEVFRSYFVVHHQQEQEAGSAAPADPEN-VTLPLQPSTMGQGVRQLAILGDDINRRY 89
 :||:::||::||::||::||::||::||::||:

Db 73 nmelqrmiadvdtspre-vff-rvaadmfadgnfwrgrvvalfyaskvlvkalcctkvp 130
 :||:::||::||::||::||::||::||::||:
QY 90 DSFFQTMLQHLOPHTAEWAYEFYFKIASLPESG-INMGRVALLGFYSRLLAHIIYRGFLT 148
 :::::||::||::||::||::||::||::||:

Db 131 elirtmgwtldf-lterllvwlqdggwegllsyfgtqtvtwgtifvagvitastltwk 189
 :::::||::||::||::||::||::||::||:
QY 149 GF LGQVTFRFYVDPEFLMHCIARWIARQGSGWAALNNGNP I-LNVVLVGVLVGQGVWR 207

RESULT 11
ID BAXA_HUMAN STANDARD; PRT; 192 AA.
AC QO7812;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN BAX.
GS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUETHERIA; PRIMATES.

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=B-CELL;
RX MEDLINE; 93364978.
RL OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
LA CELL 74:609-619(1993).

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: MEMBRANE.

WQSEKEL (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Aug 20 11:05:33 1997; MasPar time 8.89 Seconds
Tabular output not generated.
685.993 Million cell updates/sec

Title: >US-08-320-157-9
Description: (1-211) from US08320157.pep
Perfect Score: 1554
Sequence: 1 MASGGQGPPECEGEPAIP.....LVVLGVLLGQFVVRFFKS 211

Scoring table: PAM 150
Gap 11

Searched: 91006 seqs, 28888923 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pirl51

1:unann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 45.185; Variance 108.828; scale 0.415

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1554	100.0	211	13	cdh-2 protein - huma	1.43e-241
2	1529	98.4	211	13	Bak protein - human	3.45e-237
3	271	17.4	190	13	apoptosis regulator	1.24e-23
4	267	17.2	216	6	transforming protein	5.03e-23
5	268	17.2	233	14	BCL-x protein - rat	3.55e-23
6	268	17.2	233	14	bcl-x long - mouse	7.14e-23
7	266	17.1	233	6	transforming protein	1.43e-22
8	264	17.0	233	13	apoptosis regulator	4.08e-22
9	261	16.8	214	14	bcl-x transmembrane	5.77e-22
10	260	16.7	205	2	transforming protein	2.31e-21
11	256	16.5	206	6	transforming protein	2.31e-21
12	256	16.5	239	2	transforming protein	1.30e-20
13	251	16.2	199	2	transforming protein	1.30e-20
14	251	16.2	233	14	BCL-x long - rat	1.30e-20
15	251	16.2	236	2	transforming protein	1.30e-20
16	251	16.2	237	6	transforming protein	1.30e-20
17	249	16.0	236	14	BCL-2 - rat (fragment	2.60e-20
18	240	15.4	232	6	transforming protein	5.72e-19
19	220	14.2	192	14	programmed cell death	5.02e-16
20	208	13.4	192	13	bcl-2-associated pro	2.74e-14
21	203	13.1	218	13	bcl-2-associated pro	1.43e-13

22	187	12.0	133	14	I53295	bax - rat (fragment)	2.61e-11
23	182	11.7	154	14	I58194	gene bcl-2 protein -	1.29e-10
24	178	11.5	143	13	I38921	BAX splice form delt	4.62e-10
25	179	11.5	350	13	A47476	BCL2 homolog MCL1 -	3.36e-10
26	173	11.1	172	14	I49449	hemopoietic-specific	2.24e-09
27	117	7.5	400	10	S35958	beta-glucosidase - S	3.17e-02
28	114	7.3	177	13	S47778	NR-13 protein - qual	7.04e-02
29	107	6.9	255	5	S26032	cytochrome-c oxidase	4.33e-01
30	107	6.9	890	8	S44150	coat protein - straw	7.19e-01
31	105	6.8	560	7	S46724	hexose transport prot	7.19e-01
32	105	6.8	567	7	S31294	hexose transport pro	7.19e-01
33	105	6.8	567	11	S70110	HXT3 protein - yeast	7.19e-01
34	104	6.7	133	4	GPBP4	gop protein - satel	9.24e-01
35	103	6.6	470	2	SYP5RA	threonine synthase (1.15e+00
36	102	6.6	569	7	S50771	sugar transport prot	1.52e+00
37	103	6.6	817	1	RVGCT	RNA-directed RNA pol	1.19e+00
38	101	6.5	2007	3	B43402	myosin heavy chain-B	1.95e+00
39	99	6.4	527	16	S62484	hypothetical protein	3.17e+00
40	100	6.4	567	7	S49600	glucose transport prot	2.49e+00
41	100	6.4	567	7	S50708	sugar transport prot	2.49e+00
42	100	6.4	640	5	S23008	insulin-like growth	2.49e+00
43	98	6.3	680	10	H64206	fructose-permease II	4.04e+00
44	97	6.2	570	11	S70107	HXT7 protein - yeast	5.13e+00
45	97	6.2	570	16	S67932	hexose transporter H	5.13e+00

ALIGNMENTS

RESULT 1
ENTRY S58875 #type complete
TITLE cdn-2 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 01-Mar-1996
ACCESSIONS S58875
REFERENCE S58874
#authors Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, P.J.
#journal Nature (1995) 374:736-739
#title Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
#accession S58875
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA translation not shown
#residues 1-211 #label KIE
#cross-references EMBL:U16812
#note the nucleotide sequence was submitted to the EMBL Data Library, November 1994

SUMMARY #length 211 #molecular-weight 23411 #checksum 9485
Query Match 100.0%; Score 1554; DB 13; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.43e-241;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 masggqgpprqqeqgepalpsaeqvaqdtceevfrsvfhhqgeaagaapadpdm 60
QY 1 MASGGQGPPECEGEPAIPSAEEQVAQDTCEEVFRSVFHHQGEAAGAAPADDEM 60
Db 61 vtlplqpsstmgvgrqlaiigddinrrydsfctmlqlqptaaenayeyftkasslfe 120
QY 61 VTLPLQPSSTMGVGRQLAIIGDDINRRYDSEFTQMLQLQPTAENAYEYFTKASSLFE 120
Db 121 sginwgrvllgfsyrlalhiygrglgtflgqgtrfvdvfmhlcrlarwiagrggwaa 180
QY 121 SGINWGRVLLGFSYRLALHIYQRLGTFLGQVTRFVDFMLHLCRLARWIAQRGGWAA 180
Db 181 lnlgngplnlvllgvllgqfvvrffks 211
QY 181 LNLGNGPILNLVLLGVLLGQFVVRFFKS 211
RESULT 2

DATE	07-May-1995	#sequence_revision	01-Sep-1995	#text_change
ACCESSIONS	01-Dec-1995			
REFERENCE	S51761; S51762			
#authors	Michaelidis, T.M.			
#submission	submitted to the EMBL Data Library, November 1994			
#accession	S51761			
#status	preliminary			
#molecule_type	DNA			
#residues	1-233	#label	MIC	
#cross-references	EMBL:X82537			
REFERENCE	S51761			
#authors	Michaelidis, T.M.			
#submission	submitted to the EMBL Data Library, November 1994			
#accession	S51762			
#status	preliminary			
#molecule_type	DNA			
#residues	1-125, 189-233	#label	M12	
#cross-references	EMBL:X82537			
GENETICS				
#introns	125/3			
SUMMARY	#length	233	#molecular-weight	26130
			#checksum	6378
Query Match	17.2%;	Score	268;	DB 14;
Best Local Similarity	28.0%;	Pred. No.	3.55e-23;	
Matches	33;	Conservative	37;	Mismatches 46;
				Indels 2;
				Gaps 2;
Db	83	maavkqalreagdefelr	rrafsdltscqlh	tpgtaygsfcgvnelfrdgvnwgri
		1-125, 189-233		142
QY	71	MGQVGRGRLAIGDINR	YSEFQTMQLQHPAENAYEFT	KIASLFFSGINWGRVA
		1-233		130
Db	143	ffsggalcvsvdkemqlv	svrasiavmatyln	dh-lepwigengwgtfdvlygna
		1-125, 189-233		199
QY	131	LLGFSYRLALHIYQ	RGTLGFGQVTRFVDFMLHLCIARWIAQ	RGGWAAALNL-GNGP
		1-233		187
RESULT	6			
ENTRY	I49056	#type	complete	
TITLE	bcl-x long - mouse			
ORGANISM	#formal_name	Mus musculus	#common_name	house mouse
DATE	02-Jul-1996	#sequence_revision	02-Jul-1996	#text_change
	15-Oct-1996			
ACCESSIONS	I49056; S52866			
REFERENCE	I49055			
#authors	Fang, W.; Rivard, J.J.; Mueller, J.J.; Behrens, T.W.			
#journal	J. Immunol. (1994) 153:4388-4398			
#title	Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.			
#cross-references	MUID:95052604			
#accession	I49056			
#status	preliminary; translated from GB/EMBL/DBD			
#molecule_type	mRNA			
#residues	1-233	#label	RES	
#cross-references	EMBL:010101; NID:g506647; CDS_PID:g506648			
REFERENCE	S52866			
#authors	Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.			
#submission	submitted to the EMBL Data Library, November 1994			
#description	IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line through induction of bcl-Xl.			
#accession	S52866			
#status	preliminary			
#molecule_type	mRNA			
#residues	1-233	#label	KAM	
#cross-references	EMBL:X83574			
SUMMARY	#length	233	#molecular-weight	26132
			#checksum	5739
Query Match	17.2%;	Score	268;	DB 14;
Best Local Similarity	28.0%;	Pred. No.	3.55e-23;	
Matches	33;	Conservative	37;	Mismatches 46;
				Indels 2;
				Gaps 2;
Db	83	maavkqalreagdefelr	rrafsdltscqlh	tpgtaygsfcgvnelfrdgvnwgri
		1-125, 189-233		142
QY	71	MGQVGRGRLAIGDINR	YSEFQTMQLQHPAENAYEFT	KIASLFFSGINWGRVA
		1-233		130

```

##residues      1-69,'G','71-125,189-233 ##label B02
##cross-references GB:L20122; CDS_PID:g623237
GENETICS
#gene          GDB:BCL2L
##cross-references GDB:228079
#alternative splicing; apoptosis
FEATURE
#label MAT
#product apoptosis regulator bcl-xL #status predicted
#label MA2
#product apoptosis regulator bcl-xs #status predicted
1-125,189-233
#length 233 #molecular-weight 26063 #checksum 5340
SUMMARY
Query Match      17.0%; Score 264; DB 13; Length 233;
Best Local Similarity 28.0%; Pred. No. 1.43e-22;
Matches 33; Conservative 37; Mismatches 46; Indels 2; Gaps 2;

Db 83 maavkqalresgdfeleyrrafsdltqqlhtptatqsgfeqvneifrdgvnwgri 142
Qy 71 MGQVGRQALIGDDINRRYDSEFQTMLOHLOPTAENAYEYTKIASSLFESGINWGRV 130
Db 143 ffsfggalcvsvdkemqvlvriaawmatylnhd-lepwigenggwdfvelygna 199
Qy 131 LLGFSYRLALHYQRLGFLGQVTRFVVDFMLHHCIARWIAQRCGWAAALNL-GNGP 187

RESULT 9
ENTRY      I49057 #type complete
TITLE      bcl-x transmembrane deleted - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I49057
REFERENCE   Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#authors   J. Immunol. (1994) 153:4388-4398
#journal   Cloning and molecular characterization of mouse bcl-x in B
#title     and T lymphocytes.
#cross-references MUID:95052604
#accession I49057
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-214 ##label RES
##cross-references EMBL:U10102; NID:g506649; CDS_PID:g506650
GENETICS
#note      gene name bcl-x long
#molecule_type DNA
#length 214 #molecular-weight 23900 #checksum 9730
SUMMARY
Query Match      16.8%; Score 261; DB 14; Length 214;
Best Local Similarity 28.0%; Pred. No. 4.08e-22;
Matches 30; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

Db 83 maavkqalresgdfeleyrrafsdltqqlhtptatqsgfeqvneifrdgvnwgri 142
Qy 71 MGQVGRQALIGDDINRRYDSEFQTMLOHLOPTAENAYEYTKIASSLFESGINWGRV 130
Db 143 ffsfggalcvsvdkemqvlvriaawmatylnhd-lepwigenggw 188
Qy 131 LLGFSYRLALHYQRLGFLGQVTRFVVDFMLHHCIARWIAQRCGW 177

RESULT 10
ENTRY      TVHUB1 #type complete
TITLE      transforming protein bcl-2-beta - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
ACCESSIONS B29409
REFERENCE   Tsujimoto, Y.; Croce, C.M.
#authors   Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#journal   Analysis of the structure, transcripts, and protein products
#title     of bcl-2, the gene involved in human follicular lymphoma.

```

```

#cross-references MUID:86259760
#accession      B29409
#molecule_type mRNA
#residues       1-205 ##label TSU
GENETICS
#gene          GDB:BCL2
##cross-references GDB:119031
#map_position 18q21.33-18q21.33
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS       alternative splicing; B-cell lymphoma; follicular lymphoma;
               transforming protein
SUMMARY        #length 205 #molecular-weight 22182 #checksum 1183
Query Match      16.7%; Score 260; DB 2; Length 205;
Best Local Similarity 29.7%; Pred. No. 5.77e-22;
Matches 38; Conservative 37; Mismatches 49; Indels 4; Gaps 3;

Db 74 tpaapgaagpalspvpvvhla--lrqagddfarrvrrdfaemssqhlhtpctargfa 131
Qy 54 APADPEWVTLF-LQPSSTMGGVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYEFT 112
Db 132 tvveelfrdgvnwgriavffefggvmcvesvnrmsplvndialwmteylnrh-lhtwiq 190
Qy 113 KIASSLFESGINWGRVALLGFSYRLALHYQRLGFLGQVTRFVVDFMLHHCIARWIA 172
Db 191 dnggwvga 198
Qy 173 QRCGWAA 180

RESULT 11
ENTRY      D37332 #type complete
TITLE      transforming protein (bcl-2-beta) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
ACCESSIONS D37332
REFERENCE   Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#authors   Nucleic Acids Res. (1992) 20:4187-4192
#journal   Isolation and characterization of the chicken bcl-2 gene:
#title     expression in a variety of tissues including lymphoid and
               neuronal organs in adult and embryo.
#accession D37332
#status    preliminary; nucleic acid sequence not shown; not
               compared with conceptual translation
#molecule_type DNA
#residues    1-206 ##label EGU
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY        #length 206 #molecular-weight 22440 #checksum 5581
Query Match      16.5%; Score 256; DB 6; Length 206;
Best Local Similarity 29.7%; Pred. No. 2.31e-21;
Matches 38; Conservative 35; Mismatches 51; Indels 4; Gaps 3;

Db 75 tpaapgaagpalspvpvvhlt--lrqagddfarrvrrdfaemssqhlhtpctargfa 132
Qy 54 APADPEWVTLF-LQPSSTMGGVGRQLAIGDDINRRYDSEFQTMLOHLOPTAENAYEFT 112
Db 133 tvveelfrdgvnwgriavffefggvmcvesvnrmsplvndialwmteylnrh-lhtwiq 191
Qy 113 KIASSLFESGINWGRVALLGFSYRLALHYQRLGFLGQVTRFVVDFMLHHCIARWIA 172
Db 192 dnggwvga 199
Qy 173 QRCGWAA 180

RESULT 12
ENTRY      TVHUAL #type complete
TITLE      transforming protein bcl-2, splice form alpha - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change

```

[illegible]

MPERLH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Aug 20 11:08:18 1997; MasPar time 3.38 Seconds
Tabular output not generated. 298.086 Million cell updates/sec

Title: >US-08-320-157-21
Description: (1-88) from US08320157.pep
Perfect Score: 643
Sequence: 1 MASCGGPGPRQECGKPALP.....APWGRWDGSSPSGRHQPAL 88

Scoring table: PAM 150
Gap 11

Searched: 96640 seqs, 11439865 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: a-geneseq27

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20

Statistics: Mean 27.717; Variance 105.074; scale 0.264

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	643	100.0	88	13 R77878	Human Cdn-3.	1.98e-58
2	213	33.1	211	20 W03669	Bak-2 protein.	3.66e-12
3	213	33.1	211	13 R77876	Human Cdn-1.	3.66e-12
4	213	33.1	211	20 W03668	Bak protein.	3.66e-12
5	213	33.1	211	17 R81451	Bcl-1 apoptosis-relat	3.66e-12
6	213	33.1	211	13 R77877	Human Cdn-2.	3.66e-12
7	84	13.1	647	5 R03928	Xenopus laevis HSP (x	7.53e+00
8	83	12.9	641	8 R43004	Mature mouse sperm 70	9.13e+00
9	82	12.6	634	5 R03930	Gallus gallus HSP (ch	1.11e+01
10	81	12.6	341	18 R95830	Human interleukin-1-c	1.34e+01
11	81	12.6	459	13 R66729	Aromatic dihydrodiol/	1.34e+01
12	81	12.6	2510	14 R71007	Human neuronal calcic	1.34e+01
13	80	12.4	233	13 R64327	HSV L/ST ORF1.	1.62e+01
14	80	12.4	982	3 R13320	Murine Natural Killer	1.62e+01
15	80	12.4	1023	3 R13319	Partial Human Natural	1.62e+01
16	79	12.3	633	8 R43002	Mouse SLIP1 homologue	1.95e+01
17	78	12.1	429	8 R41746	MN protein.	2.36e+01
18	78	12.1	646	5 R03927	Rat HSP (rathsp70).	2.36e+01
19	76	11.8	501	12 R70996	Human alpha-1A adrene	3.43e+01
20	76	11.8	501	12 R90040	Human alpha-1A adrene	3.43e+01

21	76	11.8	510	7 R34574	Insulinoma-associated	3.43e+01
22	76	11.8	338	8 R44430	eryA region polypepti	3.43e+01
23	74	11.5	487	15 R88619	Phytase protein.	4.96e+01
24	74	11.5	1540	18 R81483	BRCA1 mutant from pat	4.96e+01
25	74	11.5	1852	19 R99448	BRCA1 allele #77 tran	4.96e+01
26	74	11.5	1863	19 R99440	BRCA1 allele #8403 tr	4.96e+01
27	74	11.5	1863	15 R76641	BRCA1 protein.	4.96e+01
28	74	11.5	1863	18 R81338	BRCA1 mutant from PM1	4.96e+01
29	74	11.5	1863	18 R81542	BRCA1 mutant from PM2	4.96e+01
30	74	11.5	1863	19 R97128	BRCA1, breast and ova	4.96e+01
31	74	11.5	1863	18 R81545	BRCA1 mutant from PM2	4.96e+01
32	74	11.5	1863	18 R81481	BRCA1	4.96e+01
33	74	11.5	1863	18 R81533	BRCA1 mutant from PM0	4.96e+01
34	74	11.5	1863	18 R81534	BRCA1 mutant from PM0	4.96e+01
35	74	11.5	1863	18 R81536	BRCA1 mutant from PM0	4.96e+01
36	74	11.5	1863	18 R81535	BRCA1 mutant from PM0	4.96e+01
37	74	11.5	1863	18 R81511	BRCA1 mutant from sam	4.96e+01
38	74	11.5	1863	18 R81514	BRCA1 mutant from sam	4.96e+01
39	74	11.5	1863	18 R81509	BRCA1 mutant from sam	4.96e+01
40	74	11.5	1863	18 R81519	BRCA1 mutant from sam	4.96e+01
41	74	11.5	1863	18 R81497	BRCA1 mutant from fam	4.96e+01
42	74	11.5	1863	18 R81485	BRCA1 mutant from pat	4.96e+01
43	74	11.5	1863	18 R81488	BRCA1 mutant from pat	4.96e+01
44	74	11.5	1863	18 R81490	BRCA1 mutant from pat	4.96e+01
45	74	11.5	1863	18 R81522	BRCA1 mutant from sam	4.96e+01

ALIGNMENTS

RESULT 1
ID R77878 standard; Protein; 88 AA.
AC R77878; 21-NOV-1995 (first entry)
DE Human Cdn-3.
KW Cdn-3; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
KW shock; lymphoma; eczema.
OS Homo sapiens.
PN W09515084-A.
PD 08-JUN-1995.
PF 30-NOV-1994; U13930.
PR 30-NOV-1993; US-160067.
PR 07-OCT-1994; US-320157.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC;
DR WPI: 95-215106/28.
DR N-PSDB: Q95494.
PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
PT etc.
PS Disclosure: Fig.7B-C: 66pp; English.
CC Southern blot analysis of human genomic DNA and a panel of
CC human/rodent somatic cell DNAs revealed at least 3 Cdn-related
CC genes residing on chromosomes 6, 11 and 20. Cdn-3 (R77878)
CC did not contain the structural features of Cdn-1 (R77876), Cdn-2
CC (R77877) or other Bcl-2 family members.
SQ Sequence 88 AA;

Query Match 100.0%; Score 643; DB 13; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.98e-58;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 masgggpgprgcgkpalpsaseeqvaqdmegfsaatffttisrrrrlkgrrpplqtqrw 60
|||||
QY 1 MASCGGPGPRQECGKPALPSASEEQVAQDMEGFSAAFTTTISRNRRLKGRPLPTQRW 60

Db 61 spcpsnlaapgwrgwdgsspsgrhqpai 88
|||||

QY 61 SPCPSNLAAPGWGRWDGSSPSGRHQPAL 88

RESULT 2

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ID W03669 standard; Protein; 211 AA.
AC W03669;
DE Bak-2 protein.
KW Human; Bak-2; apoptosis; latency; virus replication;
KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
KW protein interactive trapping; virucide; antitumour; diagnostic.
OS Homo sapiens.
PN W09633416-A1.
PD 24-OCT-1996.
PF 19-APR-1996; U05639.
PR 20-APR-1995; US-426529.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC;
DR WPI: 96-485886/48.
DR N-PSDB; T42139.
PT Screening for anti-viral agents - by detecting the ability of an
PT agent to disrupt the interaction of a Bak protein and a viral
PT protein
PS Disclosure; Fig 2; 24pp; English.
CC This Bak-2 protein sequence represents a bcl-1 homologue which
CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
CC protein, and is capable of modulating apoptosis. The protein may
CC be used in complete or partial form, or as an epitope tag fusion
CC protein, in a new virucide drug screening method, which involves
CC combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),
CC exposure to a test compound, and monitoring for disruption of the
CC interaction, e.g. by co-precipitation, protein interactive trapping
CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
CC replication or latency in the absence of apoptosis. Compounds which
CC inhibit the interaction may be used as virucide, antitumour or
CC diagnostic agents.
SQ Sequence 211 AA;

Query Match 33.1%; Score 213; DB 20; Length 211;
Best Local Similarity 78.0%; Pred. No. 3.66e-12;
Matches 32; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

DB 1 masggqpgprqcgcpalpsaseeqvaqdtteevfrsyvfy 41
QY 1 MASGGQPGPRQCGKRALPSASEEQVAQDMEG-FSAATFF 40

RESULT 3
ID R77876 standard; Protein; 211 AA.
AC R77876;
DE Human Cdn-1.
KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW auto-immune disease; reperfusion injury; hepatitis; osteoporosis;
KW shock; lymphoma; eczema.
OS Homo sapiens.
PN W09515084-A.
PD 08-JUN-1995.
PF 30-NOV-1994; U13930.
PR 30-NOV-1993; US-160067.
PR 07-OCT-1994; US-320157.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC;
DR WPI: 95-215106/28.
DR N-PSDB; Q95492.
PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells; proteins and antibodies, useful
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
PT etc.
PS Disclosure; Fig.3A-B; 66pp; English.
CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
CC previously isolated clone as probe. Recombinant Cdn-1 was produced
CC in Sf9 and human colon adenocarcinoma HT29 cells. Expression of
CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
CC survival in response to anti-Fas-mediated apoptosis.
SQ Sequence 211 AA;

Query Match 33.1%; Score 213; DB 20; Length 211;
Best Local Similarity 78.0%; Pred. No. 3.66e-12;
Matches 32; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

DB 1 masggqpgprqcgcpalpsaseeqvaqdtteevfrsyvfy 41
QY 1 MASGGQPGPRQCGKRALPSASEEQVAQDMEG-FSAATFF 40

RESULT 5
ID R81451 standard; Protein; 211 AA.
AC R81451;
DE 02-JUL-1996 (first entry)
DE Bcl-2 apoptosis-related protein.
KW Bcl-2; apoptosis; cell proliferation; cell death; diagnosis;
KW therapy.
OS Homo sapiens.
FH Key
FT Domain
FT /label= C-terminal_domain
FT /note= "putative membrane localisation sequence"
PN W09605232-A1.
PD 22-FEB-1996.
PF 09-AUG-1995; U10103.
PR 09-AUG-1994; US-287427.
PR 11-OCT-1994; US-321071.
PA (IMMU-) IMMUNOGEN INC.

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Chittenden TD;
WPI; 96-139648/14.
N-PSDB; T17375.
New isolated human Bcl-Y protein - used to develop prods. for
treating disorders characterised by inappropriate cell proliferation
or cell death
Claim 3; Fig 4; 100pp; English.
Bcl-Y protein (R81451) is a member of the Bcl-2 family and can
induce apoptosis in cells and function as a negative regulator of
Cdn-2 function. Bcl-Y mRNA was detected in all human tumour cell
lines examined and is also widely expressed in primary human
tissues. It can be obt'd. by expression of a full-length cDNA
clone (T17375) in pref. mammalian host cells. Bcl-Y can be used to
develop prods. for treating disorders associated with inappropriate
cell proliferation or cell death, and to raise antibodies used for
the diagnosis or monitoring of such disorders.
Sequence 211 AA;

Query Match 33.1%; Score 213; DB 17; Length 211;
Best Local Similarity 78.0%; Pred. No. 3.66e-12;
Matches 32; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Db 1 masqggppprqcgcpalpsaseeqvaqdtteefrsyfy 41
|||||
Qy 1 MASGGGPPPRQCGCKPALPSASEEQVAQDMEG-FSAATFF 40

RESULT 6
ID R77877 standard; Protein; 211 AA.
AC R77877;
DT 21-NOV-1995 (first entry)
DE Human Cdn-2.
KW Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
KW shock; lymphoma; eczema.
OS Homo sapiens.
FN M09515084-A.
PD 08-JUN-1995.
PF 30-NOV-1994; UI3930.
PR 30-NOV-1993; US-160067.
PR 07-OCT-1994; US-320157.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC;
DR WPI; 95-215106/28.
PR N-PSDB; Q95493.
PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
PT etc.
PS Disclosure; Fig.5D-E; 66pp; English.
CC Cdn-2 cDNA was isol'd. from a human placental genomic library
CC using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
CC in mouse progenitor B-cell F5.12 cells decreased IL-3-induced
CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
CC with Cdn-1 (R77876).
SQ Sequence 211 AA;

Query Match 33.1%; Score 213; DB 13; Length 211;
Best Local Similarity 78.0%; Pred. No. 3.66e-12;
Matches 32; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Db 1 masqggppprqcgcpalpsaseeqvaqdtteefrsyfy 41
|||||
Qy 1 MASGGGPPPRQCGCKPALPSASEEQVAQDMEG-FSAATFF 40

RESULT 7
ID R03928 standard; Protein; 647 AA.
AC R03928;
DT 30-AUG-1990 (first entry)
DE Xenopus laevis HSP (X170).
OS Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
KW Xenopus laevis.

PA (OTTA-) OTTAWA CIVIC HOSPITAL.
 PI Faulds DH, Lingwood CA, Tanphaichitr N;
 DR WPI; 93-368422/46.
 PT Mammalian fertilisation decrease for detecting and treating
 PT infertility - using sulpho glyco lipid immobilising protein
 PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma
 PT infection treatment
 PS Claim 2 and Claim 17; Page 60-62; 77pp; English.
 CC The likelihood of mammalian fertilisation is decreased by contacting
 CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/
 CC sulphated glyco-moiety interfering composition. The interfering
 CC compsn. is e.g. the heat shock 70kd protein, SLIP1 (or analogues
 CC such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid
 CC sequence R43002) or the 74.5kd mycoplasma protein (R43003).
 SQ Sequence 641 AA;

Query Match 12.9%; Score 83; DB 8; Length 641;
 Best Local Similarity 26.3%; Pred. No. 9.13e+00;
 Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 264 rtacerarrtllsstqasleldsfegldfytsitrar 301
 QY 11 ROECKPALPSASEEQVAQDMEG-FSAATFFTTISNR 47

RESULT 9
 ID R03930 standard; Protein; 634 AA.
 AC R03930;
 DT 30-AUG-1990 (first entry)
 DE Gallus gallus HSP (chkhsap70).
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 OS Gallus gallus.
 FH Key Location/Qualifiers
 FT Misc_difference 634
 FT /note= "residue given as "O" in specification"
 PN W03002564-A.
 PD 22-MAR-1990.
 PF 12-SEP-1989; 03955.
 PR 12-SEP-1988; US-243474.
 PA (CODO-) Codon.
 PI Dragon E, Faulds D, Sias S.
 DR WPI; 90-115820/15.
 PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
 PS Disclosure; Fig 2.1-2.14; 86pp; English.
 CC According to the legend of Fig 2, the G. gallus HSP sequence has
 CC 635 amino acid residues, the sequence itself has only 634,
 CC including "O" (?) at position 634.
 CC Fig. 2 provides an alignment of heat shock proteins from a variety
 CC of organisms: 1. M.hyponeumoniae (Mhysp70 - R03922);
 CC 2. Bacillus megaterium (Bmehsap70 - R03923);
 CC 3. E. coli (dnak - R03924);
 CC 4. T. cruzi (tc70kd - R03925);
 CC 5. T. cruzi (R03926);
 CC 6. Rat rattus (rathsp70 - R03927);
 CC 7. Xenopus laevis (xl70 - R03928);
 CC 8. Homo sapiens (hunhsap70 - R03929);
 CC 9. Gallus gallus (chkhsap70 - R03930);
 CC 10. Zea mays (mzehsap70 - R03931);
 CC 11. Serattia marcescens (smahsp70 - R03932).
 CC The proteins having homology to hsp's of T. cruzi can be used in
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species.
 SQ Sequence 634 AA;

Query Match 12.8%; Score 82; DB 5; Length 634;
 Best Local Similarity 26.3%; Pred. No. 1.11e+01;
 Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 267 rtacerarrtllsstqasleldsfegldfytsitrar 304
 QY 11 ROECKPALPSASEEQVAQDMEG-FSAATFFTTISNR 47

RESULT 10
 ID R95830 standard; Protein; 341 AA.
 AC R95830;
 DT 28-OCT-1996 (first entry)
 DE Human interleukin-1-converting enzyme-like apoptosis protease-3.
 KW ICE-LAP-3; interleukin-1-converting enzyme-like apoptosis protease;
 KW enzyme; Alzheimer's disease; Parkinson's disease; septic shock;
 KW head injury; rheumatoid arthritis.
 OS Homo sapiens.
 PN W09613603-A1.
 PD 09-MAY-1996.
 PF 06-JUN-1995; U07235.
 PR 01-NOV-1994; US-334251.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Hastings GA, He W, Hudson PL, Rosen CA;
 DR WPI; 96-239509/24.
 DR N-PSDB; T15276.
 PT Human ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis
 PT and treatment of Alzheimer's disease, Parkinson's disease,
 PT rheumatoid arthritis, septic shock and head injury
 PS Claim 1; Page 91-92; 67pp; English.
 CC This ICE-LAP-3 protein may be used therapeutically, e.g. as an
 CC antitumor or antiviral agent and to control embryonic development
 CC and tissue homeostasis. The protein can also be used to treat
 CC immunosuppression disorders, such as AIDS, by targeting virus
 CC infected cells for cell death. The DNA may find use in gene
 CC therapy applications.
 SQ Sequence 341 AA;

Query Match 12.6%; Score 81; DB 18; Length 341;
 Best Local Similarity 40.0%; Pred. No. 1.34e+01;
 Matches 12; Conservative 8; Mismatches 6; Indels 4; Gaps 3;

Db 49 lkgpqtlaeerretvvpaaalp-pwerwq 77
 QY 49 LKGRPLPTQRW--S-PCPSNLAAPWGRWD 75

RESULT 11
 ID R66729 standard; Protein; 459 AA.
 AC R66729;
 DT 02-OCT-1995 (first entry)
 DE Aromatic dihydrodiol/catechol deoxygenase #1.
 KW Dihydrodiol; catechol; microbial fermentation; E.coli; aromatic;
 KW deoxygenase; hydrocarbon; engineering plastic; polymerisation inhibitor;
 KW synthetic resin; drug synthesis.
 OS Pseudomonas fluorescens SD805.
 PN J06343474-A.
 PD 20-DEC-1994.
 PF 10-JUN-1993; 165163.
 PR 10-JUN-1993; JP-165163.
 PA (SHOW) SHOWA DENKO KK.
 DR WPI; 95-069306/10.
 DR N-PSDB; 079907.
 PT Prep'n of an aromatic cyclic di:hydro:diol cpd and a catechol cpd
 PT - using microbial cells transformed by DNA coding for enzyme
 PT protein sequences
 PS Claim 1; Page 8-9; 13pp; Japanese.
 CC The enzymes (R66729-34), encoded by genes Q79907-12, are involved in the
 CC synthesis of dihydrodiol and catechol compounds by microbial fermentation.
 CC in E.coli at normal temps. and pressures from aromatic hydrocarbons.
 CC The sequence presented here is of an aromatic deoxygenase of 459 amino
 CC acids. The aromatic dihydrodiol can be used as a raw material for
 CC engineering plastics and the catechol compound is used as a
 CC polymerisation inhibitor of synthetic resin and as an intermediate in
 CC drug synthesis.
 SQ Sequence 459 AA;

Query Match 12.6%; Score 81; DB 13; Length 459;
 Best Local Similarity 30.0%; Pred. No. 1.34e+01;
 Matches 18; Conservative 13; Mismatches 26; Indels 3; Gaps 3;

Db 298 tkqpaaerakerlqk-vlp-a-drmvqhmtifptcsflpsintvrtwhprgpnneivws 354
 QY 2 ASGGGPPPPROCCGKRALPFSASEQVAODMEGFSAAFTTTISRRRLKGRPLPTQRWS 61

RESULT 12
 ID R71007 standard; Protein; 2510 AA.
 AC R71007;
 DT 01-DEC-1995 (first entry)
 DE Human neuronal calcium channel subunit alpha 1A-1.
 KW Calcium channel subunit; antagonist; agonist; diagnosis;
 LW Lambert Eaton Syndrome.
 OS Homo sapiens.
 PN W09504822-A.
 PD 16-FEB-1995.
 PF 11-AUG-1994; U09230.
 PR 11-AUG-1993; US-105536.
 PR 05-NOV-1993; US-149097.
 PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
 DR WPI: 95-090900/12.
 DR N-PSDB; Q84659.

PT DNA encoding human calcium channel sub-unit(s) - used for
 developing prods. for studying calcium channels, e.g. for
 obtaining agonists and antagonists
 PT Claim 34: Page 178-190; 285pp; English.
 PS The primary transcript of the alpha 1A subunit gene is
 CC alternatively spliced to yield at least two variant mRNAs.
 CC One form, alpha 1A-1 is given in Q84659/R71007, and the other,
 CC alpha 1A-2 is given in Q84660/R71008. Alpha 1A-2 differs from
 CC alpha 1A-1 encoding sequence at the 3' end in that it lacks a
 CC 5 nt. sequence. This deletion shifts the reading frame and
 CC introduces a translation termination codon resulting in an
 CC alpha 1A-2 coding sequence that encodes a shorter alpha 1A
 CC subunit than that encoded by alpha 1A-1. DNA doncding alpha
 CC 1A subunits can be isolated using all or a portion of the DNA
 CC having sequence Q84661, Q85659 or Q84660 or DNA obtd from
 CC the phage lysate of an E. coli host contg. DNA encoding an alpha
 CC 1A subunit that has been deposited in the ATCC under accession
 CC no. 75293. The DNA is such a phage includes the DNA fragment
 CC having the sequence in Q84661 which selectively hybridises under
 CC conditions of high stringency to DNA encoding alpha 1A DNA but not
 CC to DNA encoding alpha 1B.
 SQ Sequence 2510 AA;

Query Match 12.6%; Score 81; DB 14; Length 2510;
 Best Local Similarity 31.8%; Pred. No. 1.34e+01;
 Matches 14; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Db 2235 aqerpdhgrardgrwrspsgrhmrhgssvsgspaps 2278
 QY 44 SRNRRLKGRPLPTQRWSPCPSNLAAPWGRWDGSSPSGRHQA 87

RESULT 13
 ID R64327 standard; Protein; 233 AA.
 AC R64327;
 DT 04-AUG-1995 (first entry)
 DE HSV L/ST ORF1.
 KW HSV; junction-spanning transcript; L/ST; therapy; virucide.
 OS Herpes simplex virus type 1.
 PN W09428156-A.
 PD 08-DEC-1994.
 PF 20-MAY-1994; U05770.
 PR 20-MAY-1993; US-065146.
 PA (DAND) DNA FARBER CANCER INST INC.
 PI Schaffer PA, Yen L;
 DR WPI: 95-022825/03.
 DR N-PSDB; Q76209.

PT Herpes Simplex Virus (HSV) specific junction spanning transcript
 PT - for inhibiting HSV L/ST synthesis, in the treatment of HSV
 PT infection.
 PS Disclosure; Page 34-35; 64pp; English.

CC In HSV-1, 4 intron-less open reading frames (ORFs) are present
 CC within the sequence specifying the L/ST junction-spanning
 CC transcript. ORF1-4 are given in Q76209-12, and encoded
 CC proteins in R64327-30. Antibodies raised against such proteins
 CC may be used to identify therapeutic agents.
 SQ Sequence 233 AA;

Query Match 12.4%; Score 80; DB 13; Length 233;
 Best Local Similarity 32.5%; Pred. No. 1.62e+01;
 Matches 13; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

Db 75 arrrrrrcaavtrrrrrrrgrrkreggwgsgappg 114
 QY 44 SRNRRLKGRPLPTQRWSPCPSNLAAPW-GRWDGSSPSFG 82

RESULT 14
 ID R13320 standard; Protein; 982 AA.
 AC R13320;
 DT 22-OCT-1991 (first entry)
 DE Murine Natural Killer receptor.
 KW NK; cytotoxic drugs; tumour cell.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Protein 8..982
 FT /label= mature_NK_receptor
 FT Peptide 1..7
 FT /label= partial_signal_peptide
 PN US7535206-A.
 PD 09-JUL-1991.
 PF 08-JUN-1990; 143578.
 PR 08-JUN-1990; US-535206.
 PA (USSH) NAT INST OF HEALTH.
 PI Ortaldo J, Young H, Anderson S;
 DR WPI: 91-245694/33.
 DR N-PSDB; Q13115.

PT DNA encoding a natural killer cell receptor - used to develop
 PT prods. for the immuno-detection and immuno-therapy of tumours
 PS Disclosure; Fig 2; 30pp; English.
 CC Overlapping clones, which make up the cDNA sequence from which this
 CC sequence was deduced, were isolated from a murine PBL cDNA library
 CC prepared in lambda gt10. The purified protein can mediate the
 CC cytolytic activity of mammalian cells. It specifically distinguishes
 CC tumour cells making it a candidate for the development of products
 CC for the immunodetection and immunotherapy of tumours.
 CC See also Q13114.
 SQ Sequence 982 AA;

Query Match 12.4%; Score 80; DB 3; Length 982;
 Best Local Similarity 38.2%; Pred. No. 1.62e+01;
 Matches 13; Conservative 9; Mismatches 8; Indels 4; Gaps 4;

Db 377 qrlrayrpp-sgekws-kdklsdpcssrwders 408
 QY 47 RRLKG-RPPLPTQRWSPCPSNLAAPWGRWDGSS 78

RESULT 15
 ID R13319 standard; Protein; 1023 AA.
 AC R13319;
 DT 22-OCT-1991 (first entry)
 DE Partial Human Natural Killer receptor.
 KW NK; cytotoxic drugs; tumour cell.
 OS Homo sapiens.
 PN US7535206-A.
 PD 09-JUL-1991.
 PF 08-JUN-1990; 143578.
 PR 08-JUN-1990; US-535206.
 PA (USSH) NAT INST OF HEALTH.
 PI Ortaldo J, Young H, Anderson S;
 DR WPI: 91-245694/33.
 DR N-PSDB; Q13114.

PT DNA encoding a natural killer cell receptor - used to develop

PT prods. for the immuno-detection and immuno-therapy of tumours
 PS Disclosure; Fig 1; 30pp; English.
 CC Overlapping clones, which make up the cDNA sequence from which this
 CC sequence was deduced, were isolated from a cDNA library prepared
 CC from human NK cells purified from human peripheral blood. The
 CC purified protein can mediate the cytolytic activity of mammalian
 CC cells. It specifically distinguishes tumour cells making it a
 CC candidate for the development of products for the immunodetection
 CC and immunotherapy of tumours. See also Q13115.
 SQ Sequence 1023 AA;
 Query Match 12.4%; Score 80; DB 3; Length 1023;
 Best Local Similarity 38.2%; Pred. NO. 1.62e+01;
 Matches 13; Conservative 9; Mismatches 8; Indels 4; Gaps 4;
 Db 410 qrlrayrpp-sgekws-k-gdklsdpcsrwdr 441
 Qy 47 RRLKG-RPPLPTQRWSPCPNLAAAP-WGRWDGSS 78
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 Job time : 25 secs.

M P E R L F
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Aug 20 11:09:01 1997; MasPar time 5.05 Seconds
Tabular output not generated. 503.601 Million cell updates/sec

Title: >US-08-320-157-21
Description: (1-88) from US08320157.pep
Perfect Score: 643
Sequence: 1 MASGGGPGPPROECKPALP.....APWGRWDGSSPSGRHQPAL 88

Scoring table: PAM 150
Gap 11

Searched: 91006 seqs, 2888923 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 37.327; Variance 80.459; scale 0.464

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	213	33.1	211	13	cdn-2 protein - huma	9.18e-20
2	213	33.1	211	13	Bak protein - human	9.18e-20
3	95	14.8	196	9	heat shock protein Y	1.35e-01
4	89	13.8	596	13	Shb protein - human	7.82e-01
5	86	13.4	643	7	heat shock protein 7	1.84e+00
6	85	13.2	488	10	globulin 1 - eastern	2.43e+00
7	85	13.2	651	7	heat shock cognate p	2.43e+00
8	84	13.1	636	7	70k heat shock cognate	3.21e+00
9	84	13.1	639	7	heat shock protein S	3.21e+00
10	84	13.1	640	7	heat shock cognate p	3.21e+00
11	84	13.1	642	3	heat shock protein S	3.21e+00
12	84	13.1	643	7	heat shock protein 7	3.21e+00
13	84	13.1	647	3	heat shock protein 7	3.21e+00
14	84	13.1	655	7	heat shock protein 7	3.21e+00
15	84	13.1	1878	8	genome polyprotein -	3.21e+00
16	84	13.1	2142	13	MHC class III histoc	4.23e+00
17	83	12.9	208	16	heat shock protein 7	4.23e+00
18	83	12.9	281	9	copy control protein	4.23e+00
19	83	12.9	284	12	regulatory protein G	4.23e+00
20	83	12.9	462	5	alpha-L-fucosidase (4.23e+00
21	83	12.9	638	7	heat shock protein 7	4.23e+00

22	83	12.9	640	7	A29160	heat shock protein,	4.23e+00
23	83	12.9	641	14	I56574	heat shock protein 7	4.23e+00
24	83	12.9	641	14	I54542	heat shock protein 7	4.23e+00
25	83	12.9	641	7	A45871	heat shock protein H	4.23e+00
26	83	12.9	641	7	S35718	heat shock protein H	4.23e+00
27	83	12.9	642	7	JH0095	heat shock protein 7	4.23e+00
28	83	12.9	2647	13	A37098	gelation factor ABP-	4.23e+00
29	82	12.8	209	16	S48025	heat shock protein -	5.56e+00
30	82	12.8	405	15	A61181	homeotic protein HOX	5.56e+00
31	82	12.8	634	7	A25646	heat shock protein 7	5.56e+00
32	82	12.8	639	7	JC11391	heat shock protein 7	5.56e+00
33	82	12.8	645	12	I51129	heat shock protein H	5.56e+00
34	82	12.8	651	11	JC4786	heat shock cognate p	5.56e+00
35	82	12.8	656	7	A48439	heat shock protein H	5.56e+00
36	82	12.8	814	7	S31211	collagen alpha 1(XIV	5.56e+00
37	82	12.8	874	4	Q0BE15	BSLF1 protein - huma	5.56e+00
38	82	12.8	1747	7	A45974	collagen alpha 1(XIV	5.56e+00
39	81	12.6	214	7	A03309	heat shock-related 7	7.30e+00
40	81	12.6	641	7	JN0668	heat shock cognate p	7.30e+00
41	81	12.6	644	7	A45635	heat shock protein h	7.30e+00
42	81	12.6	654	7	S27004	heat shock protein 7	7.30e+00
43	80	12.4	171	11	PQ0475	pistil extensin-like	9.56e+00
44	80	12.4	645	7	S41372	heat shock protein -	9.56e+00
45	80	12.4	656	7	S51712	heat shock protein 7	9.56e+00

ALIGNMENTS

RESULT 1
ENTRY S58875 #type complete
TITLE cdn-2 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change
S58875
REFERENCE Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky,
S.R.; Tomei, L.D.; Barr, P.J.
#journal Nature (1995) 374:736-739
#title Modulation of apoptosis by the widely distributed Bcl-2
homologue Bak.
#accession S58875
#status preliminary; nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-211 #label KIE
##cross-references EMBL:U16812
##note the nucleotide sequence was submitted to the EMBL Data
Library, November 1994

SUMMARY #length 211 #molecular-weight 23411 #checksum 9485
Query Match 33.1%; Score 213; DB 13; Length 211;
Best Local Similarity 78.0%; Pred.No. 9.18e-20;
Matches 32; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
Db 1 masggpgpprpgcgepalpsaseeqvaqtteevfrsyvf 41
|||||
QY 1 MASGGGPGPPRQCGRPALESSEQVAQDMEG-FSAATFF 40
RESULT 2
ENTRY S58873 #type complete
TITLE Bak protein - human
ALTERNATE_NAMES bcl-2 homolog; cdn-1 protein
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change
S58873
REFERENCE Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington,
C.; Lutz, R.J.; Evan, G.I.; Guild, B.C.
#journal Nature (1995) 374:733-736
#title Induction of apoptosis by the Bcl-2 homologue Bak.

```

#accession S58873
#status Preliminary: nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-211 ##label CHI
#cross-references EMBL:U23765

REFERENCE
#authors Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martinou, J.C.; Brown, R.
#journal Nature (1995) 374:731-733
#title Cloning of a bcl-2 homologue by interaction with adenovirus ElB 19K.

#accession S58872
#status Preliminary
#molecule_type mRNA
#residues 1-211 ##label FAR
#cross-references EMBL:X84213

REFERENCE
#authors Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, P.J.
#journal Nature (1995) 374:736-739
#title Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.

#accession S58874
#status Preliminary
#molecule_type mRNA
#residues 1-211 ##label KIE
#cross-references EMBL:U16811

GENETICS
#gene GDB:BAK-LSB
#cross-references GDB:635887
SUMMARY
#length 211 #molecule-weight 23409 #checksum 801

Query Match 33.18; Score 213; DB 13; Length 211;
Best Local Similarity 78.08; Pred.No. 9.18e-20;
Matches 32; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Db 1 masggggpprrqcgcpalpsaseeqvaqdtteefvsyvf 41
| | | | | | | | | | | | | | | | | | | | | |
QY 1 MASGQGPPRRQCGKPALPSASEEQVAQDMEG-FSAATFF 40
| | | | | | | | | | | | | | | | | | | | | |

RESULT 3
ENTRY 3
TITLE #type complete
ORGANISM heat shock protein y - Escherichia coli
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-Nov-1996

ACCESSIONS A40623; A56688; S28460
REFERENCE A40623
#authors Missiakas, D.; Georgopoulos, C.; Raina, S.
#journal J. Bacteriol. (1993) 175:2613-2624
#title The Escherichia coli heat shock gene htpY: mutational analysis, cloning, sequencing, and transcriptional regulation.

#cross-references MUID:93239687
#accession A40623
#status Preliminary
#molecule_type DNA
#residues 1-196 ##label MIS
#cross-references NCBI:130422; NCBI:130423
#note sequence extracted from NCBI backbone
REFERENCE A56688
#authors James, R.; Dean, D.O.; Debbage, J.
#journal DNA Seq. (1993) 3:327-332
#title Five open reading frames upstream of the dnaK gene of Escherichia coli.

#accession A56688
#status Preliminary
#molecule_type DNA
#residues 36-196 ##label JAM
#cross-references EMBL:X67700
GENETICS
#gene htpY; htpA

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[illegible]

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#cross-references MUID:89128457
#accession S25438
##status translation not shown
##molecule_type DNA
##residues 1-642 ##label SLA
##cross-references EMBL:X12926
##note This sequence has been revised in reference S42164
REFERENCE
S42164
#authors Slater, M.R.
#submitted to the EMBL Data Library, June 1993
#accession S42164
##molecule_type DNA
##residues 1-207,'S',209-417,'P',419-421,'S',423-642 ##label SL2
##cross-references EMBL:X12926
##note this is a revision to the sequence from reference S20133
GENETICS
#gene LISTA:SSAL; YG100
#map_position IL
CLASSIFICATION #superfamily heat shock protein 70
KEYWORDS heat shock; molecular chaperone; stress-induced protein; transmembrane protein
FEATURE
193-209 #domain transmembrane #status predicted #label TMM
SUMMARY #length 642 #molecular-weight 69767 #checksum 6411
Query Match 13.1%; Score 84; DB 3; Length 642;
Best Local Similarity 26.3%; Pred. No. 3-2le+00;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;
Db 261 rtacerakrtlssstgatlseidslfegdvfytsitrar 298
| | : : : : | : : : : : | : : : : |
QY 11 RQCGKPALPSASEEQVAQDMEG-FSAATFFTTISNR 47

RESULT 12
ENTRY S25585 #type complete
TITLE heat shock protein 70 - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
03-Aug-1995
ACCESSIONS S34625; S25585
REFERENCE S34625
#authors Dezeure, F.; Vaiman, M.; Chardon, P.
#journal Biochim. Biophys. Acta (1993) 1174:17-26
#title Characterization of a polymorphic heat shock protein 70 gene in swine outside the SLA major histocompatibility complex.
#accession S34625
##status preliminary
##molecule_type mRNA
##residues 1-643 ##label DEZ
##cross-references EMBL:X68213
CLASSIFICATION #superfamily heat shock protein 70
SUMMARY #length 643 #molecular-weight 71109 #checksum 9470
Query Match 13.1%; Score 84; DB 7; Length 643;
Best Local Similarity 26.3%; Pred. No. 3-2le+00;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;
Db 266 rtacerakrtlssstgatlseidslfegdvfytsitrar 303
| | : : : : | : : : : : | : : : : |
QY 11 RQCGKPALPSASEEQVAQDMEG-FSAATFFTTISNR 47

RESULT 13
ENTRY HHXL70 #type complete
TITLE heat shock protein 70 - African clawed frog
ALTERNATE_NAMES heat shock protein X16
ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 28-May-1986 #sequence_revision 28-May-1986 #text_change
15-Nov-1996
ACCESSIONS A03310; A22175
REFERENCE A90993
#authors Bienz, M.
```

```

#journal      EMBO J. (1984) 3:2477-2483
#title        Xenopus hsp 70 genes are constitutively expressed in injected
               oocytes.
#cross-references MUID:85076567
#accession     A03310
#molecule_type DNA
##residues     1-647 #label BIE
REFERENCE      A22175
#authors       Bienz, M.
#journal       Proc. Natl. Acad. Sci. U.S.A. (1984) 81:3138-3142
#title         Developmental control of the heat shock response in Xenopus.
#cross-references MUID:84221917
#accession     A22175
#molecule_type mRNA
##residues     81-120 #label B12
COMMENT        This protein is expressed constitutively in oocytes, disappears
               after fertilization, and is induced by heat shock in somatic
               cells from the gastrula stage onward.
CLASSIFICATION #superfamily heat shock protein 70
KEYWORDS       heat shock; molecular chaperone; stress-induced protein
SUMMARY        #length 647 #molecular-weight 70915 #checksum 3965

Query Match      13.1%; Score 84; DB 3; Length 647;
Best Local Similarity 26.3%; Pred. No. 3.21e+00;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 265 rtacdraktlsssqasieidsifegidfytaitar 302
Qy 11 ROECGPALPSASEQVAQDMEG-FSAATFTTISRNR 47

RESULT 14
ENTRY   S18349 #type complete
TITLE   heat shock protein 70 - carrot
ORGANISM #formal_name Daucus carota #common_name carrot
DATE     04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
         12-Apr-1995
ACCESSIONS S18349; S15514
REFERENCE   S18349
#authors    Lin, X.; Chern, M.; Zimmerman, J.L.
#journal     Plant Mol. Biol. (1991) 17:1245-1249
#title       Cloning and characterization of a carrot hsp70 gene.
#cross-references MUID:92032789
#accession   S18349
#molecule_type DNA
##residues   1-655 #label LIN
##cross-references EMBL:X60088
CLASSIFICATION #superfamily heat shock protein 70
SUMMARY        #length 655 #molecular-weight 72051 #checksum 2153

Query Match      13.1%; Score 84; DB 7; Length 655;
Best Local Similarity 30.6%; Pred. No. 3.21e+00;
Matches 11; Conservative 14; Mismatches 9; Indels 2; Gaps 2;

Db 272 eraqrtlsssta-qttleidslyegvdfyttitar 306
Qy 13 ECGPAPLPSASEQVAQDMEG-FSAATFTTISRNR 47

RESULT 15
ENTRY   S26369 #type complete
TITLE   genome polyprotein - eastern equine encephalomyelitis virus
CONTAINS nonstructural protein NS1; nonstructural protein NS2;
          nonstructural protein NS3
ORGANISM #formal_name eastern equine encephalomyelitis virus
DATE      06-Jan-1994 #sequence_revision 01-Nov-1996 #text_change
          01-Nov-1996
ACCESSIONS S26369
REFERENCE   S26369
#authors    Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V.
#journal     Mol. Gen. Microbiol. Virusol. (1991) 5:8-15
#title       Complete nucleotide sequence of the eastern equine
               encephalomyelitis virus genome.

```

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#accession     S26369
#molecule_type mRNA
##residues     1-1878 #label VOL
##cross-references EMBL:X63135
##note          sequence could not be checked because of bad print in
               paper
KEYWORDS       nonstructural protein; polyprotein
FEATURE        1-532
               533-1326
               1327-1878
               #product nonstructural protein NS1 #status predicted
               #label NS1\
               #product nonstructural protein NS2 #status predicted
               #label NS2\
               #product nonstructural protein NS3 #status predicted
               #label NS3
SUMMARY        #length 1878 #molecular-weight 208582 #checksum 5340

Query Match      13.1%; Score 84; DB 8; Length 1878;
Best Local Similarity 33.9%; Pred. No. 3.21e+00;
Matches 19; Conservative 14; Mismatches 19; Indels 4; Gaps 4;

Db 1774 pspsqd-srptpsasashtfdlftdsvaeiledfsrpfqlseikpapr 1828
Qy 7 PGPPRQCGKPALPSASEQVAQDMEGF-SAATFTTISRNR-R-LKGRPPLPTQR 59

Search completed: Wed Aug 20 11:09:37 1997
Job time : 36 secs.

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WQSRH (TM)

Release 2.1b John F. Collins, BioComputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Aug 20 11:09:54 1997; MasPar time 3.60 Seconds
Tabular output not generated. 517.994 Million cell updates/sec

Title: >US-08-320-157-21
Description: (1-88) from US08320157.ppe
Perfect Score: 643
Sequence: 1 MASGQGGPPRQECGKALP.....APWRWDGSSPSGRHQPAL 88

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 38.620; Variance 68.467; scale 0.564

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	95	14.8	196	5	HTGA_ECOLI	HEAT SHOCK PROTEIN HT
2	86	13.4	643	5	HS76_HUMAN	HEAT SHOCK 70 KD PROT
3	85	13.2	651	5	HS76_DROME	HEAT SHOCK 70 KD PROT
4	84	13.1	379	5	HS7X_PIG	HEAT SHOCK 70 KD PROT
5	84	13.1	631	5	HS73_BOVIN	HEAT SHOCK 70 KD PROT
6	84	13.1	638	5	HS72_YEAST	HEAT SHOCK PROTEIN SS
7	84	13.1	640	5	HS7C_DICDI	HEAT SHOCK COGNATE PR
8	84	13.1	641	5	HS7L_YEAST	HEAT SHOCK PROTEIN SS
9	84	13.1	643	5	HS76_PIG	HEAT SHOCK 70 KD PROT
10	84	13.1	647	5	HS70_XENLA	HEAT SHOCK 70 KD PROT
11	84	13.1	649	5	HS70_BLAEM	HEAT SHOCK 70 KD PROT
12	84	13.1	655	5	HS70_DAUCA	HEAT SHOCK 70 KD PROT
13	84	13.1	2142	1	BAT2_HUMAN	LARGE PROLINE-RICH PR
14	83	12.9	284	4	GOLI_DROME	GOLIATH PROTEIN (G1 P
15	83	12.9	462	4	FUCO_RAT	ALPHA-L-FUCOSIDASE PR
16	83	12.9	641	5	HS71_HUMAN	HEAT SHOCK 70 KD PROT
17	83	12.9	641	5	HS71_PIG	HEAT SHOCK 70 KD PROT
18	83	12.9	641	5	HS71_RAT	HEAT SHOCK 70 KD PROT
19	83	12.9	642	5	HS71_MOUSE	HEAT SHOCK 70 KD PROT
20	83	12.9	642	5	HS72_PICAN	HEAT SHOCK PROTEIN 70
21	83	12.9	2647	1	ABP2_HUMAN	ENDOTHELIAL ACTIN-BIN
22	82	12.8	634	5	HS70_CHICK	HEAT SHOCK 70 KD PROT

RESULT	ID	HTGA_ECOLI	STANDARD:	PRT:	196 AA.		
1							
23	82	12.8	639	5	HS7A_PARLI	HEAT SHOCK 70 KD PROT	1.31e+00
24	82	12.8	787	8	RIR1_HSVBC	RIBONUCLEOSIDE-DIPHOS	1.31e+00
25	82	12.8	874	10	UL52_EBV	HELICASE/PRIMASE COMP	1.31e+00
26	82	12.8	1888	2	CAIE_CHICK	COLLAGEN ALPHA 1(XIV)	1.31e+00
27	81	12.6	214	5	HS7A_DROSI	HEAT SHOCK 70 KD PROT	1.80e+00
28	81	12.6	322	5	HS70_ONCVO	HEAT SHOCK 70 KD PROT	1.80e+00
29	81	12.6	641	5	HS7A_DROME	HEAT SHOCK 70 KD PROT	1.80e+00
30	81	12.6	644	5	HS70_BRUMA	HEAT SHOCK 70 KD PROT	1.80e+00
31	81	12.6	654	5	HS70_HYDMA	HEAT SHOCK 70 KD PROT	1.80e+00
32	80	12.4	641	5	HS72_DROME	MAJOR HEAT SHOCK 70 K	2.47e+00
33	80	12.4	643	5	HS71_DROME	MAJOR HEAT SHOCK 70 K	2.47e+00
34	80	12.4	643	5	HS71_SCHPO	PROBABLE HEAT SHOCK P	2.47e+00
35	80	12.4	644	5	HS71_HANPO	HEAT-SHOCK PROTEIN 70	2.47e+00
36	80	12.4	650	5	HS71_LYCES	HEAT SHOCK COGNATE 70	2.47e+00
37	80	12.4	655	5	HS74_CANAL	HEAT SHOCK PROTEIN SS	2.47e+00
38	80	12.4	1403	6	NKCR_HUMAN	NK-TUMOR RECOGNITION	2.47e+00
39	80	12.4	1466	6	NKCR_MOUSE	NK-TUMOR RECOGNITION	2.47e+00
40	80	12.4	1822	11	YM68_CAEEL	HYPOTHETICAL HELICASE	2.47e+00
41	79	12.3	95	10	VE3_BP2	PROBABLE E3 PROTEIN.	3.38e+00
42	79	12.3	408	11	YHGL_ECOLI	HYPOTHETICAL 45.1 KD	3.38e+00
43	79	12.3	633	5	HS72_MOUSE	HEAT SHOCK-RELATED 70	3.38e+00
44	79	12.3	639	5	HS72_HUMAN	HEAT SHOCK-RELATED 70	3.38e+00
45	79	12.3	651	5	HS7C_PETHY	HEAT SHOCK COGNATE 70	3.38e+00
					ALIGNMENTS		

ALIGNMENTS

RESULT 1
ID HTGA_ECOLI STANDARD; PRT; 196 AA.
AC P28697;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).
GN HTGA OR HTPY.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94003405.
RA JAMES R., DEAN D.O., DEBBAGE J.;
RL DNA SEQ. 3:327-332(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 93239687.
RA MISSIAKAS D., GEORGOPOULOS C., RAINA S.;
RL J. BACTERIOL. 175:2613-2624(1993).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 92334977.
RA YURA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA N.,
RA ISONO K., MIZOBUCHI K., NAKATA A.;
RL NUCLEIC ACIDS RES. 20:3305-3308(1992).
CC -!- FUNCTION: NOT KNOWN, REQUIRED FOR HIGH-TEMPERATURE GROWTH OF
CC TRANSCRIPTION OF THE RPOH GENE OR THE ACTIVITY OF ITS GENE PRODUCT
CC SIGMA-32. PLAYS A ROLE OPPOSITE THAT OF DNAK, DNAJ, AND GRPE IN
CC TERMS OF HEAT SHOCK REGULATION, ANTAGONIZING THE NEGATIVE OF
CC THESE AND THUS FINE-TUNING THE HEAT SHOCK RESPONSE.
CC -!- INDUCTION: INDUCED AT HIGH TEMPERATURES.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-36 IS THE INITIATOR.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT.
DR EMBL; X67700; G41757; ALT_INIT.
DR EMBL; L03720; G290451; -.
DR EMBL; D10483; -; NOT_ANNOTATED_CDS.
DR PIR; S28460; S28460.
DR PIR; A40623; A40623.
DR ECGENE; EGI1509; HTGA.
KW HEAT SHOCK.

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FT DOMAIN          57      65      POLY-SER.
SQ SEQUENCE       196 AA; 21225 MW; D9E3CEC8 CRC32;

Query Match          14.8%; Score 95; DB 5; Length 196;
Best Local Similarity 57.1%; Pred. No. 1.66e-02;
Matches 12; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 14 ppsapaprakpcpstliaawvr 34
   |||:| ||||| |||:|
QY 53 PPLPTQRWSPCPSPNLAAPWGR 73

RESULT 2
ID HS76_HUMAN STANDARD; PRT; 643 AA.
AC P17066;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B').
GN HSPA6 OR HSP70B'.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE; 90226304.
RA LEUNG T.K.C., RAJENDRAN M.Y., MONFRIES C., HALL C., LIM L.;
RL BIOCHEM. J. 267:125-132(1990).
RN [2]
RP SEQUENCE OF 1-250 FROM N.A.
RX MEDLINE; 92128997.
RA LEUNG T.K.C., HALL C., RAJENDRAN M., SPURR N.K., LIM L.;
RL GENOMICS 12:74-79(1992).
CC -!- INDUCTION: ONLY AT HIGHER TEMPERATURES, AND NO BASAL EXPRESSION.
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; X51757; G35222; -.
DR EMBL; X51758; G35224; -.
DR EMBL; S78631; -: NOT_ANNOTATED_CDS.
DR PIR; S09036; S09036.
DR HSPF; P19120; INGA.
DR HSC-2DPAGE; P17066; HUMAN.
DR MIM; 140555; -.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
SQ SEQUENCE 643 AA; 70854 MW; D7C64887 CRC32;

Query Match          13.4%; Score 86; DB 5; Length 643;
Best Local Similarity 26.8%; Pred. No. 3.58e-01;
Matches 11; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

Db 263 glrtacerakrtlsstqtatleldsfegvdfytsitrar 303
   |||:| |||:| |||:| |||:|
QY 8 GPPROECGKPALPSAEQVAQDMEG-FSAATFFTTISNR 47

RESULT 3
ID HS7D_DROME STANDARD; PRT; 651 AA.
AC P11147;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN COGNATE 4 (HEAT SHOCK 70 KD PROTEIN 88E).
GN HSC4 OR HSC70-4.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93292982.
RA RUBIN D.M., MEHTA A., ZHU J., SHOHAM S., CHEN X., WELLS Q.,
RA PALTER K.B.;

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RL GENE 128:155-163(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90258915.
RA PERKINS L.A., DOCTOR J.S., ZHANG K., STINSON L., PERRIMON N.,
RA CRAIG E.A.;
RL MOL. CELL. BIOL. 10:3232-3238(1990).
RN [3]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE; 84005511.
RA CRAIG E.A., INGOLIA T.D., MANSEAU L.J.;
RL DEV. BIOL. 99:418-426(1983).
RN [4]
RP SEQUENCE OF 580-592.
RC STRAIN-VALLECAS; TISSUE=WING IMAGINAL DISCS;
RX MEDLINE; 93272852.
RA SANTAREN J.F., VAN DAMME J., PUTPE M., VANDEKERCKHOVE J.,
RA GARCIA-BELLIDO A.;
RL EXP. CELL RES. 206:220-226(1993).
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: LOCALISED TO A MESHWORK OF CYTOPLASMIC
CC FIBRES AROUND THE NUCLEUS. TRANSLOCATES TO THE NUCLEUS AFTER
CC THERMAL STRESS.
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; L01500; G157661; -.
DR EMBL; M36114; G157665; -.
DR EMBL; J02569; G157678; ALT_SEQ.
DR PIR; A36333; A36333.
DR HSPF; P19120; IATR.
DR FLYBASE; FBGN0001219; HSC70-4.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; HEAT SHOCK; NUCLEAR PROTEIN; MULTIGENE FAMILY.
FT CONFLICT 167 167 L -> P (IN REF. 2).
FT CONFLICT 170 170 L -> P (IN REF. 2).
FT CONFLICT 625 625 P -> G (IN REF. 2).
SQ SEQUENCE 651 AA; 71131 MW; 75CC8721 CRC32;

Query Match          13.2%; Score 85; DB 5; Length 651;
Best Local Similarity 26.3%; Pred. No. 4.97e-01;
Matches 10; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

Db 264 rtacerakrtlsstqtasleldsfegtdfytsitrar 301
   |||:| |||:| |||:| |||:|
QY 11 ROECGKPALPSAEQVAQDMEG-FSAATFFTTISNR 47

RESULT 4
ID HS7X_PIG STANDARD; PRT; 379 AA.
AC P34934;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN (FRAGMENT).
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE; 90371455.
RA BUCHMAN T.G., CABIN D.E., VICKERS S.;
RL SURGERY 108:559-566(1990).
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; M29506; G164495; -.
DR HSPF; P19120; INGA.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
RN NON_TER 1 1

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SQ SEQUENCE 379 AA; 42289 MW; 9E26ABE8 CRC32;
Query Match 13.1%; Score 84; DB 5; Length 379;
Best Local Similarity 26.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 4 rtacerakrtlsstqatleidslfevgdfytsitrar 41
QY 11 RQECGKPALPSASEEQVAQDMEG-FSAATFTTISRNR 47

RESULT 5
ID HS73_BOVIN STANDARD; PRT; 631 AA.
AC P34933;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN 3.
GN HSP70-3.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
[1]
RN SEQUENCE FROM N.A.
RA GROSZ M.D., MASSEY V.K., SKOW L.C.;
RL SUBMITTED (XXX-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC OF NEWLY TRANSLATED POLYPEPTIDES AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; L10428; G163161; -.
DR HSP; P19120; INGSJ.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; CHAPERONE; HEAT SHOCK; MULTIGENE FAMILY.
SQ SEQUENCE 631 AA; 69199 MW; C7B8B580 CRC32;

Query Match 13.1%; Score 84; DB 5; Length 631;
Best Local Similarity 23.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Db 257 aparltacerakrtlsstqatleidslfevgdfytsitrar 299
QY 6 GPGPRQECGKPALPSASEEQVAQDMEG-FSAATFTTISRNR 47

RESULT 6
ID HS72_YEAST STANDARD; PRT; 638 AA.
AC P10592;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HEAT SHOCK PROTEIN SSA2.
GN SSA2 OR YL024C OR L0931.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
[1]
RN SEQUENCE FROM N.A.
RA STRAIN-S288C;
RX MEDLINE; 89128457.
RL SLATER M.N., CRAIG E.A.;
RL NUCLEIC ACIDS RES. 17:805-806(1989).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX PORNELLE B., GORFEAU A.;
RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
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RN SEQUENCE OF 71-638 FROM N.A.
RA DUESTERHOEFF A., FLOETH M., HEUSS-NEITZEL D., HILBERT H., MOESTL D.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
[4]
RN SEQUENCE OF 91-97 AND 325-341.
RC STRAIN-S288C;
RX MEDLINE; 95203288.
RA GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,
RA VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
RL FEMS MICROBIOL. LETT. 137:1-8(1996).
[5]
RN SEQUENCE OF 186-195.
RC STRAIN-ATCC 38531 / Y41;
RA NORBECK J., BLONBERG A.;
RL ELECTROPHORESIS 15:1466-1486(1994).
[6]
RN ACETYLATION, AND PHOSPHORYLATION.
RA GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,
RA VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
RL SUBMITTED (SEP-1994) TO THE SWISS-PROT DATA BANK.
CC -1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; X12927; G4546; -.
DR EMBL; Z73129; E245749; -.
DR EMBL; X97560; E238712; -.
DR PIR; S20139; S20139.
DR HSP; P19120; IATR.
DR SWISS-2DPAGE; P10592; YEAST.
DR YEPD; 9800; -.
DR LISTA; SC01203; SSA2.
DR SGD; L0002070; SSA2.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW HEAT SHOCK; ATP-BINDING; MULTIGENE FAMILY; ACETYLATION;
KW PHOSPHORYLATION.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 638 AA; 69338 MW; 676F4EE3 CRC32;

Query Match 13.1%; Score 84; DB 5; Length 638;
Best Local Similarity 26.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 260 rtacerakrtlsstqatleidslfevgdfytsitrar 297
QY 11 RQECGKPALPSASEEQVAQDMEG-FSAATFTTISRNR 47

RESULT 7
ID HS7C_DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;
OC EUMYCETOZOA; DICTYOSTELIA.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-AX3;
RX MEDLINE; 94008983.
RA HAUS U., TROMMLER P., FISHER P.R., HARTMANN H., LOTTSCHEICH F.,
RA NOEGEL A.A., SCHLEICHER M.;
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RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN=AX3;
RX MEDLINE; 94043116.
RA EDDY R.J., SAUTERER R.A., CONDEELIS J.S.;
RL J. BIOL. CHEM. 268:23267-23274(1993).
CC -1- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -1- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; S65739; G415582; -;
DR EMBL; X75263; G433875; -;
DR EMBL; L22736; G433180; -;
DR PIR; S37394; S37394.
DR HSP; P19120; INGA.
DR DICTYDB; DD07777; HSPB.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00325; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; CHAPERONE.
FT CONFLICT 1 29
FT MSSIGIDLTGYSCGVQWQNDRVVEIIAND ->
FT IHHINGNATWVVEGVPVLSFN (IN REF. 2).
FT N -> T (IN REF. 2).
FT V -> A (IN REF. 2).
FT R -> A (IN REF. 2).
FT S -> A (IN REF. 2).
FT V -> A (IN REF. 2).
FT I -> L (IN REF. 2).
FT F -> P (IN REF. 2).
FT CONFLICT 352 352
SQ SEQUENCE 640 AA; 70499 MW; 8550670E CRC32;

Query Match 13.1%; Score 84; DB 5; Length 640;
Best Local Similarity 26.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 262 rtacerakrtlssaqtsvelsfegldfytsitar 299
| | : : : | : : : : | : : : |
Qy 11 RQCGKPALPSAEQVAQDMEG-FSAATFTTISRNR 47

RESULT 8
ID HS71_YEAST STANDARD; PRT; 641 AA.
AC P10591;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HEAT SHOCK PROTEIN SSAL (HEAT SHOCK PROTEIN YG100).
GN SSAL OR YAL005C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE; 89128457.
RA SLATER M.R., CRAIG E.A.;
RL NUCLEIC ACIDS RES. 17:805-806(1989).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE; 95028152.
RA CLARK M.W., KENG T., STORMS R.K., ZHONG W., FORTIN N., ZENG B.,
RA DELANEY S., OUELLETTE B.F.F., BARTON A.B., KABACK D.B., BUSSEY H.;
RL YEAST 10:535-541(1994).
[3]
RP SEQUENCE OF 590-641 FROM N.A.
RX MEDLINE; 85087943.
RA OGDEN R.C., LEE M.-C., KNAPP G.;
RL NUCLEIC ACIDS RES. 12:9367-9382(1984).
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RN [4]
RP REVISIONS TO 207; 417 AND 421.
RA SLATER M.R.;
RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
[5]
RN SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE; 95203288.
RA GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,
RA VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
RL ELECTROPHORESIS 15:1466-1486(1994).
[6]
RN SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RA NORBECK J., BLOMBERG A.;
RL FEMS MICROBIOL. LETT. 137:1-8(1996).
[7]
RN ACETYLATION.
RP GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,
RA VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
RL SUBMITTED (SEP-1994) TO THE SWISS-PROT DATA BANK.
CC -1- FUNCTION: SSAL MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSAL AND SSA2 PROTEINS IS EXPECTED. SSAL CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; X12926; G312352; -;
DR EMBL; L22015; G349747; ALT_SEQ.
DR PIR; S25438; HHBYAL.
DR PIR; S42164; S42164.
DR HSP; P19120; INGI.
DR SWISS-2DPAGE; P10591; YEAST.
DR IEPD; 9788; -;
DR LISTA; SC01202; SSAL.
DR SGD; L0002069; SSAL.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW HEAT SHOCK; ATP-BINDING; MULTIGENE FAMILY; ACETYLATION.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 641 AA; 69526 MW; 5B23162E CRC32;

Query Match 13.1%; Score 84; DB 5; Length 641;
Best Local Similarity 26.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 260 rtacerakrtlssaqtsvelsfegldfytsitar 297
| | : : : | : : : : | : : : |
Qy 11 RQCGKPALPSAEQVAQDMEG-FSAATFTTISRNR 47

RESULT 9
ID HS76_PIG STANDARD; PRT; 643 AA.
AC Q04967;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B').
GN HSP70B'.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOCYTES;
RX MEDLINE; 93326632.
RA DEZEURE F., VAINAN M., CHARDON P.;
RL BIOCHIM. BIOPHYS. ACTA 1174:17-26(1993).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
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CC EMBL; X68213; G1978; -.
DR PIR; S25585; S25585.
DR PIR; S34625; S34625.
DR HSSP; P19120; INGI.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
SQ SEQUENCE 643 AA; 71109 MW; 6F2B78FD CRC32;

Query Match      13.1%; Score 84; DB 5; Length 643;
Best Local Similarity 26.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 266 rtacerakrtlsstgatldeidslfegvdfytsitrar 303
QY 11 RQCGKPALPSASEEQVAQDMEG-FSAATFTTISRNR 47

RESULT 10
ID HS70_XENLA STANDARD; PRT; 647 AA.
AC P02827;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN (HSP70).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85076567.
RA BIENZ M.;
RL EMBO J. 3:2477-2483(1984).
RN [2]
RP SEQUENCE OF 81-120 FROM N.A.
RX MEDLINE; 84221917.
RA BIENZ M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 81:3138-3142(1984).
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; X01102; G64796; -.
DR EMBL; K02307; G214272; -.
DR PIR; A03310; HHXL70.
DR HSSP; P19120; IATR.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; HEAT SHOCK.
SQ SEQUENCE 647 AA; 70915 MW; F8D46C32 CRC32;

Query Match      13.1%; Score 84; DB 5; Length 647;
Best Local Similarity 26.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 265 rtacdraktlsssqasieidslfegvdfytsitrar 302
QY 11 RQCGKPALPSASEEQVAQDMEG-FSAATFTTISRNR 47

RESULT 11
ID HS70_BLAEM STANDARD; PRT; 649 AA.
AC P48720;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN.
OS BLASTOCODIADIELLA EMERSONII.
OC EUKARYOTA; FUNGI; MASTIGOMYCOTINA; CHYTIDIOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95129910.
RA STEFANI R.M.; GOMES S.L.;
RL GENE 152:19-26(1995).

-!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
CC EMBL; L22497; G773670; -.
DR ATP-BINDING; CHAPERONE.
SQ SEQUENCE 649 AA; 70833 MW; 8ACFF56F CRC32;

Query Match      13.1%; Score 84; DB 5; Length 649;
Best Local Similarity 26.3%; Pred. No. 6.89e-01;
Matches 10; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

Db 267 rtacerakrtlsssaqtsieidslfegidfytisitar 304
QY 11 RQCGKPALPSASEEQVAQDMEG-FSAATFTTISRNR 47

RESULT 12
ID HS70_DAUCA STANDARD; PRT; 655 AA.
AC P26791;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE HEAT SHOCK 70 KD PROTEIN.
OS DAUCUS CAROTA (CARROT).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; APIALES;
OC UMBELLIFERAEE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92032789.
RA LIN X.; CHERN M.; ZIMMERMAN J.L.;
RL PLANT MOL. BIOL. 17:1245-1249(1991).
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; X60088; G18357; -.
DR PIR; S18349; S18349.
DR HSSP; P19120; INGT.
DR PROSITE; PS00297; HSP70_1.
DR PROSITE; PS00329; HSP70_2.
DR PROSITE; PS01036; HSP70_3.
KW ATP-BINDING; HEAT SHOCK.
SQ SEQUENCE 655 AA; 72051 MW; 791B240F CRC32;

Query Match      13.1%; Score 84; DB 5; Length 655;
Best Local Similarity 30.8%; Pred. No. 6.89e-01;
Matches 11; Conservative 14; Mismatches 9; Indels 2; Gaps 2;

Db 272 eraqrtlsssta-qttieidslyvegdfyttitrar 306
QY 13 ECGKPALPSASEEQVAQDMEG-FSAATFTTISRNR 47

RESULT 13
ID BAT2_HUMAN STANDARD; PRT; 2142 AA.
AC P48634;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-T-CELL;
RX MEDLINE; 90192810.
RA BANERJI J.; SANDS J.; STROMINGER J.L.; SPIES T.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2374-2378(1990).
RN [2]
RP SEQUENCE OF 1-1860 FROM N.A.
RX MEDLINE; 93272029.
RA IRIS F.J.M.; BOUGUELERET L.; PRIEUR S.; CATERINA D.; PRIVAS G.;
RA PERROT V.; JURKA J.; RODRIGUEZ-TOME P.; CLAVERIE J.-M.; DAUSSET J.;
RL COHEN D.;
RL NAT. GENET. 3:137-145(1993).
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 M P S R E L H
 (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Wed Aug 20 11:12:02 1997; MasPar time 5.48 Seconds
 Tabular output not generated. 438.125 Million cell updates/sec

Title: >US-08-320-157-22
 Description: (1-210) from US08320157.pap
 Perfect Score: 1554
 Sequence: 1 MASGGGPPPRQCEGPALP.....LVVLGVLLGQFVRRFFKS 210

Scoring table: PAM 150
 Gap 11

Searched: 96640 seqs, 11439865 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-genesec7
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20

Statistics: Mean 32.457; Variance 141.622; scale 0.229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1543	99.3	211	20	Bak protein.	4.01e-136
2	1543	99.3	211	17	Bcl-1 apoptosis-relat	4.01e-136
3	1543	99.3	211	13	Human Cdn-1.	4.01e-136
4	1511	97.2	211	20	Bak-2 protein.	5.36e-133
5	1511	97.2	211	13	Human Cdn-2.	5.36e-133
6	1136	73.1	152	13	Human Cdn-1(60-211).	1.82e-96
7	1061	68.3	141	13	Human Cdn-1(71-211).	3.42e-89
8	880	56.6	116	13	Human Cdn-1(96-211).	1.07e-71
9	258	16.6	190	13	Chicken lymphoid BCL.	3.49e-13
10	256	16.5	232	19	Apoptosis-blocking pr	5.25e-13
11	250	16.1	233	13	Human thymus BCL-XL.	1.79e-12
12	250	16.1	233	20	Bcl-XL protein.	1.79e-12
13	245	15.8	232	19	Apoptosis-blocking pr	4.95e-12
14	245	15.8	239	19	Apoptosis-blocking pr	4.95e-12
15	243	15.6	205	13	Human bcl-2 beta prot	7.43e-12
16	243	15.6	205	13	Human thymus BCL-2.	7.43e-12
17	243	15.6	205	13	Human bcl-2 protein.	7.43e-12
18	243	15.6	239	13	Human bcl-2 alpha pro	7.43e-12
19	243	15.6	239	9	Human oncogene bcl-2	7.43e-12
20	243	15.6	239	1	Sequence of bcl-2-ai	7.43e-12
					P80987	

21	243	15.6	239	13	R70331	Human bcl-2 protein.	7.43e-12
22	243	15.6	239	8	R42312	Bcl-2 oncogene produc	7.43e-12
23	213	13.7	88	13	R7878	Human Cdn-3.	3.14e-09
24	213	13.7	205	1	P80988	Sequence of bcl-2-bet	3.14e-09
25	204	13.1	192	13	R71407	Murine Bax protein.	1.88e-08
26	203	13.1	229	19	W01021	Apoptosis-blocking pr	2.29e-08
27	194	12.5	192	13	R71406	Human Bax protein.	1.36e-07
28	179	11.5	350	12	R68814	Human mcl-1 gene prod	2.55e-06
29	150	9.7	63	13	R68885	Human thymus BCL-XL.	6.50e-04
30	98	6.3	277	14	R76996	Deduced sequence enco	7.07e+00
31	97	6.2	170	13	R68888	Human thymus BCL-XS.	8.35e+00
32	96	6.2	443	19	W05298	Esterase secretory pr	9.86e+00
33	94	6.0	338	14	R73955	Duffy blood group gpD	1.37e+01
34	91	5.9	2749	3	R13887	Inositol-3-phosphate	2.24e+01
35	89	5.7	277	14	R74737	ACT-4 cell surface re	3.10e+01
36	89	5.7	277	15	R79904	ACT-4-h-1 receptor se	3.10e+01
37	88	5.7	912	14	R79163	Partial sequence of b	3.10e+01
38	88	5.7	912	13	R82658	Human mGluR4.	3.64e+01
39	88	5.7	2695	20	W07632	Human type I inositol	3.64e+01
40	88	5.7	2713	19	W00168	Human T cell inositol	3.64e+01
41	88	5.7	451	14	R79909	N. crassa mtr gene pr	4.27e+01
42	87	5.6	470	9	R47118	Mtr protein of Neuros	4.27e+01
43	87	5.6	1984	18	R99639	Peripheral nervous sy	4.27e+01
44	87	5.6	1989	18	R92317	Peripheral nervous sy	4.27e+01
45	87	5.6					

ALIGNMENTS

RESULT 1
 ID W03668 standard; Protein; 211 AA.
 AC W03668; 1997 (first entry)
 DE Bak protein.
 KW Human; Bak; apoptosis; latency; virus replication;
 KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.
 OS Homo sapiens.
 PN W09633416-A1.
 PD 24-OCT-1996.
 PF 19-APR-1996; U05639.
 PR 20-APR-1995; US-426529.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI; 96-485886/48.
 DR N-PSDB: T42138.
 PT Screening for anti-viral agents - by detecting the ability of an agent to disrupt the interaction of a Bak protein and a viral protein
 PT protein
 PS Disclosure; Fig 1; 24pp; English.
 CC This Bak protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents.
 CC diagnostic agents.
 CC Sequence 211 AA;
 SQ

Query Match 99.3%; Score 1543; DB 20; Length 211;
 Best Local Similarity 99.5%; Pred. No. 4.01e-136;
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Db 1 masgggppprqcegpalsaseeqvaqgteevfrsyvfrhqqeqeagvaapadpem 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1 MASGGGPPPRQCEGPALPSASEEQVAQDTEEVFRSYVFRHQQEQEAGVAAPDPEM 60

Db 61 vtllpqpstmgvgrqlaigddinrrydsfqtmlqlhqlptaeayeyftkiatslfe 120
 Qy 61 VTLPLQPSSTMGVGRQLAIIIGDDINRRYDSEFQTMQLHQLPTAEAYEYFTKIATSLFE 120
 Db 121 sginwgrvllgfyrylalhvyqhlgtflgqvtrfvdmlhchiarwlaqrggwvaa 180
 Qy 121 SG-NWGRVVALLGFGYRLALHVVYQHLGTFLGQVTRFVDFMLHHCIARWIAQRGWVAA 179
 Db 181 lnlgngpnlvllgfvllgqvrrffks 211
 Qy 180 LNLGNGPILNLVLLGVLLGQFVVRFFKS 210

RESULT 2
 ID R81451 standard; Protein; 211 AA.
 AC R81451;
 DT 02-JUL-1996 (first entry)
 DE Bcl-2 apoptosis-related protein.
 KW Bcl-2; apoptosis; cell proliferation; cell death; diagnosis;
 KW therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 188..205
 FT /label= C-terminal_domain
 FT /note= "putative membrane localisation sequence"
 PN W09605232-A1.
 PD 22-FEB-1996.
 PF 09-AUG-1995; U10103.
 PR 09-AUG-1994; US-287427.
 PR 11-OCT-1994; US-321071.
 PA (IMMU-) IMMUNOGEN INC.
 PI Chittenden TD;
 DR WPI: 96-139648/14.
 DR N-PSDB: T17375.
 PT New isolated human Bcl-2 protein - used to develop prods. for
 PT treating disorders characterised by inappropriate cell proliferation
 PT or cell death
 PS Claim 3; Fig 4; 100pp; English.
 CC Bcl-2 protein (R81451) is a member of the Bcl-2 family and can
 CC induce apoptosis in cells and function as a negative regulator of
 CC Bcl-2 function. Bcl-2 mRNA was detected in all human tumour cell
 CC lines examined and is also widely expressed in primary human
 CC tissues. It can be obtd. by expression of a full-length cDNA
 CC clone (T17375) in pref. mammalian host cells. Bcl-2 can be used to
 CC develop prods. for treating disorders associated with inappropriate
 CC cell proliferation or cell death, and to raise antibodies used for
 CC the diagnosis or monitoring of such disorders.
 SQ Sequence 211 AA;

Query Match 99.3%; Score 1543; DB 17; Length 211;
 Best Local Similarity 99.5%; Pred. No. 4.01e-136;
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 masggppprqecgepalpsaseeqvadtteevfryvfhqgeaqeagvaapadpem 60
 Qy 1 MASGGPPPRQECGEPAIPSAEEQVADTEEVFRYVFRHQGEAQEAGVAAPADPEM 60
 Db 61 vtllpqpstmgvgrqlaigddinrrydsfqtmlqlhqlptaeayeyftkiatslfe 120
 Qy 61 VTLPLQPSSTMGVGRQLAIIIGDDINRRYDSEFQTMQLHQLPTAEAYEYFTKIATSLFE 120
 Db 121 sginwgrvllgfyrylalhvyqhlgtflgqvtrfvdmlhchiarwlaqrggwvaa 180
 Qy 121 SG-NWGRVVALLGFGYRLALHVVYQHLGTFLGQVTRFVDFMLHHCIARWIAQRGWVAA 179
 Db 181 lnlgngpnlvllgfvllgqvrrffks 211
 Qy 180 LNLGNGPILNLVLLGVLLGQFVVRFFKS 210

RESULT 4
 ID W03669 standard; Protein; 211 AA.
 AC W03669;
 DT 22-FEB-1997 (first entry)
 DE Bak-2 protein.
 KW Human; Bak-2; apoptosis; latency; virus replication;
 KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.
 OS Homo sapiens.
 PN W09633416-A1.
 PD 24-OCT-1996.
 PF 19-APR-1996; U05639.
 PR 20-APR-1995; US-426529.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 96-485886/48.
 DR N-PSDB: T42139.
 PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 PS Disclosure; Fig 2; 24pp; English.
 CC This Bak-2 protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
 CC protein, and is capable of modulating apoptosis. The protein may

DT 21-NOV-1995 (first entry)
 DE Human Cdn-1.
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
 KW shock; lymphoma; eczema.
 OS Homo sapiens.
 PN W09515084-A.
 PD 08-JUN-1995.
 PF 30-NOV-1994; U13930.
 PR 30-NOV-1993; US-160067.
 PR 07-OCT-1994; US-320157.
 PA (LARB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 95-215106/28.
 DR N-PSDB: Q95492.
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure; Fig. 3A-B; 66pp; English.
 CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
 CC previously isolated clone as probe. Recombinant Cdn-1 was produced
 CC in Sf9 and human colon adenocarcinoma Hs29 cells. Expression of
 CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
 CC survival in response to anti-Fas-mediated apoptosis.
 SQ Sequence 211 AA;

Query Match 99.3%; Score 1543; DB 13; Length 211;
 Best Local Similarity 99.5%; Pred. No. 4.01e-136;
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 masggppprqecgepalpsaseeqvadtteevfryvfhqgeaqeagvaapadpem 60
 Qy 1 MASGGPPPRQECGEPAIPSAEEQVADTEEVFRYVFRHQGEAQEAGVAAPADPEM 60
 Db 61 vtllpqpstmgvgrqlaigddinrrydsfqtmlqlhqlptaeayeyftkiatslfe 120
 Qy 61 VTLPLQPSSTMGVGRQLAIIIGDDINRRYDSEFQTMQLHQLPTAEAYEYFTKIATSLFE 120
 Db 121 sginwgrvllgfyrylalhvyqhlgtflgqvtrfvdmlhchiarwlaqrggwvaa 180
 Qy 121 SG-NWGRVVALLGFGYRLALHVVYQHLGTFLGQVTRFVDFMLHHCIARWIAQRGWVAA 179
 Db 181 lnlgngpnlvllgfvllgqvrrffks 211
 Qy 180 LNLGNGPILNLVLLGVLLGQFVVRFFKS 210

RESULT 4
 ID W03669 standard; Protein; 211 AA.
 AC W03669;
 DT 22-FEB-1997 (first entry)
 DE Bak-2 protein.
 KW Human; Bak-2; apoptosis; latency; virus replication;
 KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
 KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
 KW protein interactive trapping; virucide; antitumour; diagnostic.
 OS Homo sapiens.
 PN W09633416-A1.
 PD 24-OCT-1996.
 PF 19-APR-1996; U05639.
 PR 20-APR-1995; US-426529.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 PI Barr PJ, Kiefer MC;
 DR WPI: 96-485886/48.
 DR N-PSDB: T42139.
 PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 PS Disclosure; Fig 2; 24pp; English.
 CC This Bak-2 protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
 CC protein, and is capable of modulating apoptosis. The protein may

PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure: Fig.11; 66pp; English.
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
 CC activity, suggesting that small, truncated Cdn-1 molecules may be
 CC potent therapeutics.
 SQ Sequence 141 AA;

Query Match 68.3%; Score 1061; DB 13; Length 141;

Best Local Similarity 99.3%; Pred. No. 3.42e-89;

Matches 140; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 mgvqrglaigddinrrydsfctmlqhlqtaenayeftkiatalfesginwgrvva 60
 QY 71 MGQVGRQLAIGDDINRRYDSFCTMLQHLQPTAENAYEFTKIATSLFESG-NMGRVVA 129
 Db 61 llfggyralhvyqhgltgflgqvtrfvdfmhlhclarwiagrgvwaalnlgngpilm 120
 QY 130 LLFGGYRLALHVVYQHGTLGFLGQVTRFVDFMLHCLARWIAGRGVWAALNLGNGPILN 189
 Db 121 vlvlvgvllgqfvvrrffks 141
 QY 190 VLVLGVVLLGQFVVRFFKS 210

RESULT 8

ID R77881 standard; Protein; 116 AA.

AC R77881;

DE 21-NOV-1995 (first entry)

Human Cdn-1(96-211).

CC Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;

CC autoimmune disease; reperfusion injury; hepatitis, osteoporosis;

CC shock; lymphoma; eczema.

OS Homo sapiens.

PN WO9515084-A.

PD 08-JUN-1994.

PF 30-NOV-1994; UI3930.

PR 30-NOV-1993; US-160067.

PR 07-OCT-1994; US-320157.

PA (LXRB-) LXR BIOTECHNOLOGY INC.

PI Barr PJ, Kiefer MC;

PI WPI; 95-215106/28.

PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.

PS Disclosure: Fig.11; 66pp; English.

CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in

CC increased cell survival in response to anti-Fas-mediated apoptosis.

CC Truncated Cdn-1 derivatives given in R77879-81 were used to

CC test the effects of deleting the N-terminal sequences of Cdn-1

CC on this activity.

SQ Sequence 116 AA;

Query Match

Best Local Similarity 56.6%; Score 880; DB 13; Length 116;

Matches 115; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 mlqlhqltaenayeftkiatlsfsginwrvallgfygrylhyqhgltgflqvvt 60
 QY 96 MLQHLQPTAENAYEFTKIATSLFESG-NMGRVALLGFGYRLALHYQHGLTGFLQVVT 154
 Db 61 rfvydfmlhclarwiagrgvwaalnlgngpilmvlvgvllgfvvrrffks 116
 QY 155 RFVYDFMLHCLARWIAGRGVWAALNLGNGPILNLVLVLGVLLGQFVVRFFKS 210

RESULT 9

ID R68884 standard; Protein; 190 AA.

R68884;
 AC 10-AUG-1995 (first entry)
 DE Chicken lymphoid BCL-X.
 KW Chicken; bird; fowl; BCL-X; apoptosis; cell death; cancer;
 KW neurodegenerative disease; autoimmune disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; multiple sclerosis; oncogene.
 PN WO9500642-A.
 PS Callus domesticus.
 PD 05-JAN-1995.
 PF 22-JUN-1994; U07089.
 PR 22-JUN-1993; US-081448.
 PA (ARCH-) ARCH DEV CORP.
 PA (UNMI) UNIV MICHIGAN.
 PI Boise LH, Nunez G, Thompson CB;
 DR WPI; 95-052079/07.
 DR N-PSDB; Q81696.
 PT New polynucleotide encoding new poly-peptide(s) that modify
 PT apoptosis - and related vectors, recombinant cells and
 PT antibodies, useful in assay and for control of cell death in e.g.
 PT neuronal cells, lymphocytes and cancers
 PS Claim 4; Page 87; 127pp; English.
 CC This protein may be expressed recombinantly, particularly with pcmv
 CC plasmids as vectors for expression in mammalian cell cultures.
 CC The protein has particular application in cancer cells (failure of
 CC programmed cell death (PCD)) or neurodegenerative and autoimmune diseases
 CC (premature PCD), e.g. Parkinson's disease, amyotrophic lateral
 CC sclerosis and multiple sclerosis.
 SQ Sequence 190 AA;
 Query Match 16.6%; Score 258; DB 13; Length 190;
 Best Local Similarity 28.2%; Pred. No. 3.49e-13;
 Matches 37; Conservative 32; Mismatches 59; Indels 3; Gaps 3;
 Db 60 vvnqatvhrssilevheivrasdvuqalrdaqdefelrlyrafsdltsqhltgtaqsf 119
 QY 52 VAAPADPEMVTLPQPSTMGVGRQLAIGDDINRRYDSFCTMLQHLQPTAENAYEFT 111
 Db 120 eqvvnelfhdgvnwgrivaffsgfgalcvsvdkemrviwgriwvmtlytdh-ldpwi 178
 QY 112 TKIATSLFESG-NMGRVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHCLARWI 170
 Db 179 qenggwvrtal 189
 QY 171 AQRGGWV-AAL 180
 RESULT 10
 ID W01020 standard; Protein; 232 AA.
 AC W01020;
 DE 18-DEC-1996 (first entry)
 DE Apoptosis-blocking protein Bcl-2 mutant 80-6 (del80-86).
 KW Apoptosis-regulating protein; Bcl-2; oncogene;
 KW adenovirus E1B 19K protein; cell death; cancer; tumour;
 KW immune disorder; diagnosis; therapy; Bip1A; Bip13; Bip5; Nip1;
 KW Nip2; Nip3.
 OS Synthetic.
 PN EP-733706-A2.
 PD 25-SEP-1996.
 PF 21-MAR-1996; 104542.
 PR 21-MAR-1995; US-408095.
 PA (UYSL-) UNIV ST LOUIS.
 PI Chinnadurai G;
 DR WPI; 96-427055/43.
 PT Nucleic acids encoding apoptosis regulating proteins - useful for
 PT diagnosing and treating immune disorders, malignancies, etc.
 PS Example 8; Page 34-35; 60pp; English.
 CC The 80-6 mutant (W01020) of the bcl-2 oncogene product (W01018)
 CC lacks amino acids 80-86 of the native protein. This and other
 CC Bcl-2 mutants (see also W01019-21) were used in a two hybrid assay
 CC to examine the interactions between Bcl-2 and novel apoptosis-
 CC regulating proteins Nip1, Nip2 and Nip3 (W00997-99). 2 Motifs
 CC (W01003-04) on Bcl-2 were identified that are essential for
 CC interaction with the Nip proteins. These motifs show homology

PD 25-SEP-1996.
PF 21-MAR-1996; 104542.
PR 21-MAR-1995; US-408095.
PA (UYSL-) UNIV ST LOUIS.
EP-733706-AZ.

PI Chinnadurai G;
 DR WPI; 96-427055/43.
 PT Nucleic acids encoding apoptosis regulating proteins - useful for
 PS diagnosing and treating immune disorders, malignancies, etc.
 CC Example 8; Page 33-34; 60pp; English.
 CC The 42-8 mutant (W01019) of the bcl-2 oncogene product (W01018)
 CC lacks amino acids 42-48 of the native protein. This and other
 CC Bcl-2 mutants (see also W01020-21) were used in a two hybrid assay
 CC to examine the interactions between Bcl-2 and novel apoptosis-
 CC regulating proteins Nip1, Nip2 and Nip3 (W00997-99). The Nip
 CC proteins were unable to interact with mutant 42-8. The site of
 CC deletion in this mutant corresponds to a motif (see also W01003)
 CC on Bcl-2 essential for interaction with Nip proteins. A second
 CC binding motif (W01004) of Bcl-2 was also identified, and both
 CC show homology to motifs (W01005-06) found on the 19K protein
 CC (W01010) of adenovirus E1B.
 SQ Sequence 232 AA;

Query Match 15.8%; Score 245; DB 19; Length 232;
 Best Local Similarity 29.3%; Pred. No. 4.95e-12;
 Matches 41; Conservative 36; Mismatches 57; Indels 6; Gaps 5;

Db 67 tpaapgaapalaspvppvhl--lrqgddfarrvrrdffaemssqlhltpftargcfa 124
 QY 54 APADPEMTLP-LQPSSTMGQVQLAIGDDINRRYDSEFTMLQLHQPFAENAYEFT 112
 Db 125 tvveelfrdgynwgrivaffefggvmcvesvnmremplvndialwmtelylnrh-lhtwiq 183
 QY 113 KIATSLFESG-NMGRVVALGFGYRLALHYQHGLTGFLGQVTRFVDFVDFMLHICIARWIA 171
 Db 184 dnggdwafvel-ygpmrpl 202
 QY 172 QRGGWAAALNLGNGPILNVL 191

RESULT 14
 ID W01018 standard; Protein; 239 AA.
 AC W01018;
 DT 18-DEC-1996 (first entry)
 DE Apoptosis-blocking protein Bcl-2.
 KW Apoptosis-regulating protein; Bcl-2; oncogene;
 KW adenovirus E1B 19K protein; cell death; cancer; tumour;
 KW immune disorder; diagnosis; therapy; Bp1A; Bp13; Bp5; Nip1;
 KW Nip2; Nip3.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Binding_site 43..51
 FT /label= Binding_motif
 FT /note= "Interacts with Bp1 proteins"
 FT Binding_site 106..112
 FT /label= Binding_motif
 FT /note= "Interacts with Bp1 proteins"
 PN EP-733706-A2.
 PD 25-SEP-1996.
 PF 21-MAR-1996; 104542.
 PR 21-MAR-1995; US-408095.
 PA (UYSL-) UNIV ST LOUIS.
 PI Chinnadurai G;
 DR WPI; 96-427055/43.
 PT Nucleic acids encoding apoptosis regulating proteins - useful for
 PS diagnosing and treating immune disorders, malignancies, etc.
 CC Example 8; Page 32-33; 60pp; English.
 CC The bcl-2 oncogene product (W01018) enhances the survival of
 CC haematopoietic B and T cells by blocking apoptosis induced by
 CC diverse agents. Its activity is similar to that of the 19K
 CC protein (W01010) of adenovirus E1B. 3 Novel proteins, Bp1A,
 CC Bp13 and Bp5 (W01000-02), that specifically interact with
 CC Bcl-2, have been identified. Mutational analysis (see also
 CC W01019-21) shows the apoptosis-regulating Nip proteins (see also
 CC W00997-99) associate with Bcl-2 at specific sites (see also
 CC W01003-04) that show homology to motifs (W01005-06) on 19K.
 SQ Sequence 239 AA;

Query Match 15.8%; Score 245; DB 19; Length 239;
 Best Local Similarity 29.3%; Pred. No. 4.95e-12;
 Matches 41; Conservative 36; Mismatches 57; Indels 6; Gaps 5;

Db 74 tpaapgaapalaspvppvhl--lrqgddfarrvrrdffaemssqlhltpftargcfa 131
 QY 54 APADPEMTLP-LQPSSTMGQVQLAIGDDINRRYDSEFTMLQLHQPFAENAYEFT 112
 Db 132 tvveelfrdgynwgrivaffefggvmcvesvnmremplvndialwmtelylnrh-lhtwiq 190
 QY 113 KIATSLFESG-NMGRVVALGFGYRLALHYQHGLTGFLGQVTRFVDFVDFMLHICIARWIA 171
 Db 191 dnggdwafvel-ygpmrpl 209
 QY 172 QRGGWAAALNLGNGPILNVL 191

RESULT 15
 ID R71405 standard; protein; 205 AA.
 AC R71405;
 DT 30-OCT-1995 (first entry)
 DE Human bcl-2 beta protein.
 KW Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KW proliferation; cell cycle progression; Bax; apoptotic cell death;
 KW hyperplasia; cytokine; death repressor; BHL; BH2; cancer therapy;
 KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
 KW ischaemic cell death.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 136..155
 FT /label= BHL_domain
 FT /note= "Represents Bax binding site"
 FT Domain 187..192
 FT /label= BH2_domain
 FT /note= "Represents Bax binding site"
 PN WO9505750-A.
 PD 02-MAR-1995.
 PF 24-AUG-1994; U09701.
 PR 26-AUG-1993; US-112208.
 PR 25-MAY-1994; US-248819.
 PA (UNIW) UNIV WASHINGTON.
 PI Korsmeyer SJ;
 DR WPI; 95-106605/14.
 PT Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.
 PS Disclosure; Page 40; 133pp; English.
 CC The sequences given in R71404-05 represent the human bcl-2 alpha and
 CC beta proteins respectively. bcl-2 is encoded by a proto-oncogene and
 CC is capable of inhibiting apoptosis in many hematopoietic cell systems.
 CC bcl-2 is a 26 kD membrane-associated cytoplasmic protein and is thought
 CC to function by enhancing the survival of hematopoietic cells of B and T
 CC origins rather than directly promoting proliferation of these cell
 CC types. bcl-2 has not been shown to directly promote cell cycle
 CC progression nor does it necessarily alter the dose response to limiting
 CC concentrations of IL-3. bcl-2 has been shown to form heterodimers with
 CC a 21 kD protein, Bax. Overexpressed Bax accelerates apoptotic cell death
 CC induced by cytokine deprivation in an IL-3 dependent cell line, and it
 CC also acts to counter the death repressor activity of bcl-2. Therefore,
 CC the ratio between bcl-2 and Bax determines cell survival or death
 CC following an apoptotic stimulus. The invention gives a mutant form of
 CC bcl-2 in which there is at least one amino acid substitution or deletion
 CC in the BHL or BH2 domains. This makes the mutant protein substantially
 CC incapable of binding Bax and/or incapable of death repressor activity.
 CC Down regulation of bcl-2 is useful in cancer therapy, controlling
 CC hyperplasias and eliminating self-reactive clones in autoimmunity by
 CC favouring death effector molecules. Up regulating bcl-2 is beneficial in
 CC treatment and diagnosis of immunodeficiency diseases, including AIDS and
 CC neurodegenerative and ischaemic cell death.
 SQ Sequence 205 AA;

Query Match 15.6%; Score 243; DB 13; Length 205;
 Best Local Similarity 29.7%; Pred. No. 7.43e-12;

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Matches 38; Conservative 36; Mismatches 49; Indels 5; Gaps 4;
Db 74 tpaaggaagpalsppvpvhl--lrqagddfsrryrgdfaemssqlhltptfgrifa l31
Qy 54 APADPEMTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTLQLHQAENAYEYFT 112
Db 132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnlalwmtaylorh-lhtwiq 190
Qy 113 KIATSLFESG-NWGRVALLGFGYRLALHVYQHGTLGFLGQVTRFVDFMLHHCIARWIA 171
Db 191 dnggwvga 198
Qy 172 ORGGWVAA 179

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Search completed: Wed Aug 20 11:12:27 1997
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W P S R L
(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Aug 20 11:12:45 1997; MasPar time 9.69 Seconds
Tabular output not generated.
626.144 Million cell updates/sec

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Perfect Score: 1554
Sequence: 1 MASGGGPGPPROCEGEPALP.....LVVLGVLLGQFVRRFFKS 210
Scoring table: PAM 150
Gap 11
Searched: 91006 seqs, 28888923 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: pif51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev
Statistics: Mean 45.070; Variance 107.726; scale 0.418

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1543	99.3	211	13	Bak protein - human	1.46e-241
2	1511	97.2	211	13	cdn-2 protein - huma	6.54e-236
3	258	16.6	190	13	apoptosis regulator	6.91e-22
4	254	16.3	233	14	BCL-X protein - rat	2.79e-21
5	254	16.3	233	14	bcl-x long - mouse	2.79e-21
6	250	16.1	233	13	apoptosis regulator	1.13e-20
7	247	15.9	214	14	bcl-x transmembrane	3.19e-20
8	246	15.8	216	6	transforming protein	4.51e-20
9	245	15.8	233	6	transforming protein	6.38e-20
10	243	15.6	205	2	transforming protein	1.27e-19
11	239	15.4	206	6	transforming protein	5.07e-19
12	239	15.4	239	2	transforming protein	5.07e-19
13	236	15.2	233	14	BCL-X-Long - rat	1.42e-18
14	234	15.1	199	2	transforming protein	2.83e-18
15	234	15.1	236	2	transforming protein	2.83e-18
16	234	15.1	237	6	transforming protein	2.83e-18
17	231	14.9	236	14	BCL-2 - rat (fragmen	7.90e-18
18	231	14.4	232	6	transforming protein	1.21e-16
19	205	13.2	192	14	programmed cell deat	5.11e-14
20	194	12.5	192	13	bcl-2-associated pro	1.93e-12
21	189	12.2	218	13	bcl-2-associated pro	9.88e-12

RESULT ENTRY	1	11.3	350	13	A47476	6.50e-10
176	11.2	133	14	I33295	bax - rat (fragment)	1.23e-09
24	167	10.7	154	14	gene bcl-2 protein -	1.12e-08
25	165	10.6	143	13	BAX splice form delt	2.09e-08
26	158	10.2	172	14	hemopoietic-specific	1.83e-07
27	116	7.5	255	5	cytochrome-c oxidase	3.59e-02
28	106	6.8	133	4	gap protein - satell	4.98e-01
29	102	6.6	400	10	beta-glucosidase - S	1.38e+00
30	102	6.6	636	14	gene NK10 protein -	1.36e+00
31	103	6.6	890	8	coat protein - straw	1.06e+00
32	98	6.3	177	13	NR-13 protein - quai	3.65e+00
33	98	6.3	206	11	phosphatidyl-N-methy	3.65e+00
34	97	6.2	170	14	bcl-x short - mouse	4.68e+00
35	96	6.2	470	2	threonine synthase (5.92e+00
36	97	6.2	912	14	metabotropic glutama	4.65e+00
37	96	6.1	2007	3	myosin heavy chain-B	5.92e+00
38	95	6.1	471	7	collagen alpha 3(IV)	7.51e+00
39	94	6.0	338	13	glycoprotein D - hum	9.52e+00
40	94	6.0	338	13	human blood group an	9.52e+00
41	94	6.0	531	10	hypothetical protein	9.52e+00
42	94	6.0	535	1	dimethylalanine mono	9.52e+00
43	94	6.0	822	11	hypothetical protein	9.52e+00
44	94	6.0	885	11	acetylglutamate kina	9.52e+00
45	94	6.0	908	14	metabotropic glutama	9.52e+00

ALIGNMENTS

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176	11.2	Bak protein - human	
24	167	bcl-2 homolog; cdn-1 protein	
25	165	#formal_name Homo sapiens #common_name man	
26	158	15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change	
27	116	06-Sep-1996	
28	106	S58873; S58872; S58874	
29	102	S58873	
30	102	Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I.; Guild, B.C.	
31	103	Nature (1995) 374:733-736	
32	98	Induction of apoptosis by the Bcl-2 homologue Bak.	
33	98	S58873	
34	97	#status preliminary; nucleic acid sequence not shown	
35	96	#molecule_type mRNA	
36	97	#residues 1-211 #label CHI	
37	96	#cross-references EMBL:U23765	
38	95	S58872	
39	94	Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martinou, J.C.; Brown, R.	
40	94	Nature (1995) 374:731-733	
41	94	Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K.	
42	94	S58872	
43	94	#status preliminary	
44	94	#molecule_type mRNA	
45	94	#residues 1-211 #label FAR	
		#cross-references EMBL:X84213	
		S58874	
		Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, P.J.	
		Nature (1995) 374:736-739	
		Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.	
		S58874	
		#status preliminary	
		#molecule_type mRNA	
		#residues 1-211 #label KIE	
		#cross-references EMBL:U16811	
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		#gene GDB:BAK-LSB	
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		#length 211 #molecular-weight 23409 #checksum 801	

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Best Local Similarity 99.5%; Pred. No. 1.46e-241;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 masgggppprgcegepalpsaseeqvqdtteevfrsyfyrhqqeaeagvaapadpem 60
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Qy 1 MASGGGPPPRGCEGEPALPSASEEQVAQDTEEVFRSYFYRHQQEAEAGVAAPADPEM 60
|||||

Db 61 vtlplqbstmqvgrqlaigddinrrydsfqlmqlqptaeayeyftkiatsife 120
|||||
Qy 61 VTLPLQBSTMQVGRQLAIGDDINRRYDSEFQMLQLQPTAEAYEYFTKIATSLFE 120
|||||

Db 121 sglngrvvallyfyrialhyqglgtqgvtfrfvdfmlhlciaarwlaqrggwaa 180
|||||
Qy 121 SG-NWGRVVALLYFYRIALHYQHGLTGFLGQVTRFVDFMLHLCIARWIAQRGGWAA 179
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Db 181 lnlgngpnlvllgqvllgfvvrrffks 211
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Qy 180 LNLGNGPILNLVLLGVLLGQFVVRFFKS 210
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RESULT 2
ENTRY      S58875      #type complete
TITLE      cdn-2 protein- human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change
01-Mar-1996
ACCESSIONS S58875
REFERENCE   S58874
#authors   Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky,
S.R.; Tomei, L.D.; Barr, P.J.
#journal   Nature (1995) 374:736-739
#title     Modulation of apoptosis by the widely distributed Bcl-2
homologue Bak.
#accession S58875
#status    preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues  1-211 #label KIE
#cross-references EMBL:U16812
#note      the nucleotide sequence was submitted to the EMBL Data
Library, November 1994
SUMMARY    #length 211 #molecular-weight 23411 #checksum 9485

Query Match      97.2%; Score 1511; DB 13; Length 211;
Best Local Similarity 96.7%; Pred. No. 6.54e-236;
Matches 204; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Db 1 masgggppprgcegepalpsaseeqvqdtteevfrsyfyrhqqeaeagvaapadpem 60
|||||
Qy 1 MASGGGPPPRGCEGEPALPSASEEQVAQDTEEVFRSYFYRHQQEAEAGVAAPADPEM 60
|||||

Db 61 vtlplqbstmqvgrqlaigddinrrydsfqlmqlqptaeayeyftkiatsife 120
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Qy 61 VTLPLQBSTMQVGRQLAIGDDINRRYDSEFQMLQLQPTAEAYEYFTKIATSLFE 120
|||||

Db 121 sglngrvvallyfyrialhyqglgtqgvtfrfvdfmlhlciaarwlaqrggwaa 180
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Qy 121 SG-NWGRVVALLYFYRIALHYQHGLTGFLGQVTRFVDFMLHLCIARWIAQRGGWAA 179
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Db 181 lnlgngpnlvllgqvllgfvvrrffks 211
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Qy 180 LNLGNGPILNLVLLGVLLGQFVVRFFKS 210
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ENTRY      A47537      #type complete
TITLE      apoptosis regulator bcl-x - chicken
ORGANISM   #formal_name Gallus gallus #common_name chicken
DATE       03-May-1994 #sequence_revision 03-May-1994 #text_change
03-May-1994
ACCESSIONS A47537
REFERENCE   A47537

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#authors      Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
               Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
               C.B.
#journal      Cell (1993) 74:597-608
#title       bcl-x, a bcl-2-related gene that functions as a dominant
               regulator of apoptotic cell death.
#accession    A47537
#status       preliminary
#molecule_type DNA
#residues     1-190 #label BOI
#cross-references GB:L20120
SUMMARY       #length 190 #molecular-weight 21467 #checksum 5509

Query Match      16.6%; Score 258; DB 13; Length 190;
Best Local Similarity 28.2%; Pred. No. 6.91e-22;
Matches 37; Conservative 32; Mismatches 59; Indels 3; Gaps 3;

Db 60 vngatvhrsslevhelvrasdrqalrdagdefelrlyrrafsdltsglhtptaygsf 119
| | | | |
Qy 52 VAAPADPEMVTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQMLQLQPTAEAYEYF 111
| | | | |

Db 120 eqvvnelfhdgvnwgriavffsggalcvesvdkemvlgvrvswmttyltdh-ldpwi 178
| | | | |
Qy 112 TKIATSLFESG-NWGRVVALLYFYRIALHYQHGLTGFLGQVTRFVDFMLHLCIARWI 170
| | | | |

Db 179 qenggwvrtal 189
| | | | |
Qy 171 AORGGWV-AAL 180
| | | | |

RESULT 4
ENTRY      S51761      #type complete
TITLE      BCL-X protein - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       07-May-1995 #sequence_revision 01-Sep-1995 #text_change
01-Dec-1995
ACCESSIONS S51761; S51762
REFERENCE   S51761
#authors    Michaelidis, T.M.
#submission submitted to the EMBL Data Library, November 1994
#accession  S51761
#status     preliminary
#molecule_type DNA
#residues   1-233 #label MIC
#cross-references EMBL:X82537
REFERENCE   S51761
#authors    Michaelidis, T.M.
#submission submitted to the EMBL Data Library, November 1994
#accession  S51762
#status     preliminary
#molecule_type DNA
#residues   1-125,189-233 #label MI2
#cross-references EMBL:X82537
GENETICS
#introns    125/3
SUMMARY     #length 233 #molecular-weight 26130 #checksum 6378

Query Match      16.3%; Score 254; DB 14; Length 233;
Best Local Similarity 25.5%; Pred. No. 2.79e-21;
Matches 36; Conservative 41; Mismatches 60; Indels 4; Gaps 4;

Db 61 dspavngatghs-ssldarevipmaavkqalreagdefelrlyrrafsdltsglhtpcta 119
| | | | |
Qy 48 EAEGVAAPADPEMVTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQMLQLQPTAE 107
| | | | |

Db 120 yqsfqevvnelfrdgvnwgriavffsggalcvesvdkemqvlvsriaswmatyindh-l 178
| | | | |
Qy 108 YEYFTKIATSLFESG-NWGRVVALLYFYRIALHYQHGLTGFLGQVTRFVDFMLHLCI 166
| | | | |

Db 179 epwigcnggdwtdfvdlygnna 199
| | | | |
Qy 167 ARWIAQRGGWVAAALNL-GNGP 186
| | | | |

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5
RESULT      5
ENTRY       I49056      #type complete
TITLE       bcl-x long - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
            15-Oct-1996
ACCESSIONS  I49056; S52866
REFERENCE   I49055
#authors    Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal     J. Immunol. (1994) 153:4388-4398
#title       Cloning and molecular characterization of mouse bcl-x in B
            and T lymphocytes.
#cross-references MUID:95052604
#accession  I49056
#status      preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues    1-233 #label RES
#cross-references EMBL:U10101; NID:g506647; CDS_PTD:g506648
REFERENCE   S52866
#authors     Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
#submission submitted to the EMBL data library, November 1994
#description IL-5 inhibits anti-IgM-induced apoptosis in an immature B
            cell line through induction of bcl-xl.
#accession  S52866
#status      preliminary
#molecule_type mRNA
#residues    1-233 #label KAM
#cross-references EMBL:X83574
SUMMARY     #length 233 #molecular-weight 26132 #checksum 5739

Query Match 16.3%; Score 254; DB 14; Length 233;
Best Local Similarity 25.8%; Pred. No. 2,79e-21;
Matches 36; Conservative 41; Mismatches 60; Indels 4; Gaps

Db 61 dspavngatghs-ssidarevipmaavkqalreagdegfelrrrafsdltsqlhitpcta 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 48 EAEGVAAPADPEWVTLPLQSPSTMGQVQQLAIGDINRRVDSFQFMQLHQLPTAENA 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 120 yqsfecvnnelfrdgwngrivaffsgalgcvesdkemqvlsvriaswmatylndh-l 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 108 YEYFKTIATSLFESG-NWGRVALLGFGYRLALRVYQHLGTGLGQVTRFVDFMLHCCI 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 179 epwliqenggwdfvdiygnaa 199
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 167 ARWIAQRGGVVAALNL-GNGP 186

RESULT      6
ENTRY       B47537      #type complete
TITLE       apoptosis regulator bcl-xL - human
ALTERNATE_NAMES bcl-2-related protein
CONTAINS       apoptosis regulator bcl-xs
ORGANISM       #formal_name Homo sapiens #common_name man
DATE          16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
            06-Sep-1996
ACCESSIONS   B47537; C47537
REFERENCE    B47537
#authors     Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
            Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
            C.B.
#journal     Cell (1993) 74:597-608
#title       bcl-x, a bcl-2-related gene that functions as a dominant
            regulator of apoptotic cell death.
#accession  B47537
#status      nucleic acid sequence not shown; translated from
            GB/EMBL/DBDJ
#molecule_type mRNA
#residues    1-233 #label BOI
#cross-references GB:L20121; CDS_PTD:Q07817
#accession  C47537
#status      nucleic acid sequence not shown; translated from
            GB/EMBL/DBDJ

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ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
15-Jun-1996
ACCESSIONS B37332
REFERENCE B37332
#authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
#accession B37332
#status preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
#molecule_type DNA
#residues 1-216 #label EGU
#cross-references EMBL:D11382
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 216 #molecular-weight 23492 #checksum 3596
Query Match 15.8%; Score 246; DB 6; Length 216;
Best Local Similarity 28.5%; Pred. No. 4.51e-20;
Matches 39; Conservative 37; Mismatches 56; Indels 5; Gaps 5;
Db 60 hrpdpssaaasevppae-glrppp-g-vhlalrqagdferryrqrdfaqmsqllht 116
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 44 QOEQAEGVAAPADPEMTLPQPSTMGVGRQLAIIGDDINRRYDSEFQTMQLQLQPT 103
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 pftagravaveelfrdgwngrivaffefggvncvesvnrmsplvndiatwmtelyn 176
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 104 AENAYEYTKIATSLFESG-NMGRVALLGFGYRLALHYQHGLTGFVGQVTRFVDFML 162
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 rh-lhnwldngdgwvra 192
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 163 HHCIARWIAQRGGWAA 179
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 9
ENTRY #type complete
TITLE transforming protein (bcl-2-alpha) - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
12-Apr-1995
ACCESSIONS A37332
REFERENCE A37332
#authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
#accession A37332
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-233 #label EGU
#cross-references EMBL:D11381
GENETICS
#introns 189/3
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS transforming protein
SUMMARY #length 233 #molecular-weight 25697 #checksum 99
Query Match 15.8%; Score 245; DB 6; Length 233;
Best Local Similarity 28.5%; Pred. No. 6.38e-20;
Matches 41; Conservative 40; Mismatches 57; Indels 6; Gaps 6;
Db 60 hrpdpssaaasevppae-glrppp-g-vhlalrqagdferryrqrdfaqmsqllht 116
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 44 QOEQAEGVAAPADPEMTLPQPSTMGVGRQLAIIGDDINRRYDSEFQTMQLQLQPT 103
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 pftagravaveelfrdgwngrivaffefggvncvesvnrmsplvndiatwmtelyn 176
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 104 AENAYEYTKIATSLFESG-NMGRVALLGFGYRLALHYQHGLTGFVGQVTRFVDFML 162
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 rh-lhnwldngdgwvra 192
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Qy 163 HHCIARWIAQRGGWAAALNL-GNG 185
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 10
ENTRY #type complete
TITLE transforming protein bcl-2-beta - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
ACCESSIONS B29409
REFERENCE A29409
#authors Tsujimoto, Y.; Croce, C.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products
of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
#accession B29409
#molecule_type mRNA
#residues 1-205 #label TSU
GENETICS
#gene GDB:BCU2
#cross-references GDB:119031
#map_position 18q21.33-18q21.33
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS alternative splicing; B-cell lymphoma; follicular lymphoma;
transforming protein
SUMMARY #length 205 #molecular-weight 22182 #checksum 1183
Query Match 15.6%; Score 243; DB 2; Length 205;
Best Local Similarity 29.7%; Pred. No. 1.27e-19;
Matches 38; Conservative 36; Mismatches 49; Indels 5; Gaps 4;
Db 74 tpaapgaagpalspvpvvhla--lrqagddfsrryrgdfaeamsqllhtpftargrfa 131
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 54 APADPEMTLP-LQPSTMGVGRQLAIIGDDINRRYDSEFQTMQLQPTAENAYEVFT 112
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132 tvveelfrdgwngrivaffefggvncvesvnrmsplvndialwmtelylnrh-lhtwiq 190
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 113 KIATSLFESG-NMGRVALLGFGYRLALHYQHGLTGFVGQVTRFVDFMLHHCIARWIA 171
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 191 dnggwvga 198
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 172 QRGGWAA 179
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 11
ENTRY #type complete
TITLE transforming protein (bcl-2-beta) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
15-Jun-1996
ACCESSIONS D37332
REFERENCE A37332
#authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
#accession D37332
#status preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
#molecule_type DNA
#residues 1-206 #label EGU
CLASSIFICATION #superfamily bcl transforming protein
SUMMARY #length 206 #molecular-weight 22440 #checksum 5581
Query Match 15.4%; Score 239; DB 6; Length 206;
Best Local Similarity 29.7%; Pred. No. 5.07e-19;
Matches 38; Conservative 34; Mismatches 51; Indels 5; Gaps 4;
Db 75 tpaapgaagpalspvpvvhlt--lrqagddfsrryrrdfeamsqllhtpftargrfa 132
:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY 54 APADPEMTLP-LQPSSTMGVGRQLAIGDDINRRYDSEFQTMQLQHLQPTAENAYEFT 112
Db 133 tvveelfrdgynwgrivaffefgvmcvesvnrmsplvndialwmteylnrh-lhtwiq 191
QY 113 KIATSLFESG-NWGRVVALGFGYRLAHVYQHGLTGLGQVTRFVDFMLHHCIARWIA 171
Db 192 dnggwvga 199
QY 172 ORGGWVAA 179

RESULT 12
ENTRY TVHUAL #type complete
TITLE transforming protein bcl-2, splice form alpha - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS A37332; A29409; S02452; A24428; A27622; B27622
REFERENCE A37332
#authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.
#accession C37332
#status nucleic acid sequence not shown; not compared with conceptual translation
##molecule_type DNA
##residues 1-239 ##label EGU
#note this report is a correction
REFERENCE A29409
#authors Tsujimoto, Y.; Croce, C.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
#accession A29409
##molecule_type mRNA
##residues 1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
#note this sequence has been corrected in reference A37332
REFERENCE S02452
#authors Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
#journal EMBO J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--Ig fusion gene in lymphoma.
#cross-references MUID:88196071
#accession S02452
##molecule_type mRNA
##residues 1-239 ##label SST
REFERENCE A24428
#authors Cleary, M.L.; Smith, S.D.; Sklar, J.
#journal Cell (1986) 47:19-28
#title Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation.
#cross-references MUID:87002488
#accession A24428
##molecule_type mRNA
##residues 1-58,'T',60-116,'R',118-239 ##label CLE
REFERENCE A27622
#authors Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
#journal Oncogene Res. (1988) 2:263-275
#title Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
#cross-references MUID:88217344
#accession A27622
##molecule_type mRNA
##residues 1-58,'T',60-239 ##label HUA
#accession B27622
##molecule_type DNA

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##residues 1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2
#note the sequence was determined from the germline gene
COMMENT Constitutive expression of BCL2 following t(14;18) chromosomal translocation is typically found in follicular lymphoma.
GENETICS
#gene GDB:BCL2
##cross-references GDB:119031
#map_position 18q21.33-18q21.33
FUNCTION
#description blocks apoptosis in hematopoietic cells
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS alternative splicing; B-cell lymphoma; follicular lymphoma; proto-oncogene; transforming protein
SUMMARY #length 239 #molecular-weight 26266 #checksum 8323
Query Match 15.4%; Score 239; DB 2; Length 239;
Best Local Similarity 29.3%; Pred. No. 5.07e-19;
Matches 41; Conservative 36; Mismatches 57; Indels 6; Gaps 5;
Db 74 tpaapgaagpalsvppvvhlt--lrqagddfsrryrrdfaemssqlhltftargfa 131
QY 54 APADPEMTLP-LQPSSTMGVGRQLAIGDDINRRYDSEFQTMQLQHLQPTAENAYEFT 112
Db 132 tvveelfrdgynwgrivaffefgvmcvesvnrmsplvndialwmteylnrh-lhtwiq 190
QY 113 KIATSLFESG-NWGRVVALGFGYRLAHVYQHGLTGLGQVTRFVDFMLHHCIARWIA 171
Db 191 dnggwdfvel-ygpsmrpl 209
QY 172 ORGGWVAAALNGLNGPILNLV 191

RESULT 13
ENTRY I67431 #type complete
TITLE BCL-X-Long - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I67431
REFERENCE I53295
#authors Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
#cross-references MUID:95129487
#accession I67431
#status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-233 ##label RES
#cross-references EMBL:U34963; NID:gl004376; CDS_PID:gl004377
SUMMARY #length 233 #molecular-weight 26122 #checksum 8310
Query Match 15.2%; Score 236; DB 14; Length 233;
Best Local Similarity 28.4%; Pred. No. 1.42e-18;
Matches 33; Conservative 30; Mismatches 50; Indels 3; Gaps 3;
Db 83 maavkqalreagdefelrrafsdltslqhltpgtvysfeqvvnelfrdgvnwgriva 142
QY 71 MGQVGRQLAIGDDINRRYDSEFQTMQLQHLQPTAENAYEFTKIATSLFESG-NWGRVAA 129
Db 143 sssfggcalcvsvdkemqivsvriaswmaylnhdh-lepwiqenggwtdtfdvlygn 197
QY 130 LLGFGYRLAHVYQHGLTGLGQVTRFVDFMLHHCIARWIAQRGGWVAAALNL-GN 184

RESULT 14
ENTRY TVMSB1 #type complete
TITLE transforming protein bcl-2-beta - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change

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02-Jun-1994
ACCESSIONS      B25960
REFERENCE        A90893
#authors        Negrini, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                  C.M.
#journal        Cell (1987) 49:455-463
#title          Molecular analysis of mbcl-2: structure and expression of the
                  murine gene homologous to the human gene involved in
                  follicular lymphoma.
#cross-references MUID:87187643
#accession      B25960
#molecule_type DNA
#residues       1-199 ##label NEG
GENETICS
#gene           BCL2
CLASSIFICATION  #superfamily bcl transforming protein
KEYWORDS        alternative splicing; transforming protein
SUMMARY         #length 199 #molecular-weight 22299 #checksum 7397

Query Match      15.1%; Score 234; DB 2; Length 199;
Best Local Similarity 31.1%; Pred. No. 2.83e-18;
Matches 32; Conservative 28; Mismatches 41; Indels 2; Gaps 2;

Db 94 lrragddfrvrrdfeamsqhltpftargrfatvveelfrdgvnwgrivaaffeggv 153
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 78 LAIGDDINRRYDSEFQTMLOHQAETAEAYEFTKATSLFESG-NWGRVVALLGFGYR 136
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 154 mcvesvremsplydnialwmtelylnrh-lhtwldnggwvga 195
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 137 LALHVGQHLGFLGQVTRFVDFMLHHCIAARQAQRGGWAA 179

RESULT 15
ENTRY          TVMSA1      #type complete
TITLE          transforming protein bcl-2-alpha - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
              02-Jun-1994
ACCESSIONS     A25960
REFERENCE       A90893
#authors       Negrini, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                  C.M.
#journal       Cell (1987) 49:455-463
#title        Molecular analysis of mbcl-2: structure and expression of the
                  murine gene homologous to the human gene involved in
                  follicular lymphoma.
#cross-references MUID:87187643
#accession      A25960
#molecule_type DNA
#residues       1-236 ##label NEG
GENETICS
#gene          BCL2
#introns       192/3
CLASSIFICATION #superfamily bcl transforming protein
KEYWORDS        alternative splicing; transforming protein
SUMMARY         #length 236 #molecular-weight 26524 #checksum 6709

Query Match      15.1%; Score 234; DB 2; Length 236;
Best Local Similarity 30.4%; Pred. No. 2.83e-18;
Matches 35; Conservative 30; Mismatches 47; Indels 3; Gaps 3;

Db 94 lrragddfrvrrdfeamsqhltpftargrfatvveelfrdgvnwgrivaaffeggv 153
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 78 LAIGDDINRRYDSEFQTMLOHQAETAEAYEFTKATSLFESG-NWGRVVALLGFGYR 136
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 154 mcvesvremsplydnialwmtelylnrh-lhtwldnggwdfvel-ygpsmrpl 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 137 LALHVGQHLGFLGQVTRFVDFMLHHCIAARQAQRGGWAAALNGLNGPIINVL 191

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Search completed: Wed Aug 20 11:13:22 1997
 Job time : 37 secs.

(E)

Result No.	Query %			DB	ID	Description	Pred. No.
	Score	Match	Length				
1	258	16.6	190	1	BCLX_CHICK	APOPTOSIS REGULATOR B	1.75e-27
2	254	16.3	233	1	BCLX_RAT	APOPTOSIS REGULATOR B	9.85e-27
3	250	16.1	233	1	BCLX_HUMAN	APOPTOSIS REGULATOR B	5.51e-26
4	245	15.8	233	1	BCL2_CHICK	APOPTOSIS REGULATOR B	4.70e-25
5	239	15.4	205	1	BCL2B_HUMAN	PROTEIN BCL-2-BETA.	6.08e-24
6	239	15.4	239	1	BCL2A_HUMAN	PROTEIN BCL-2-ALPHA.	6.08e-24
7	234	15.1	199	1	BCL2B_MOUSE	PROTEIN BCL-2-BETA.	5.08e-23
8	234	15.1	236	1	BCL2A_MOUSE	PROTEIN BCL-2-ALPHA.	5.08e-23
9	232	14.9	236	1	BCL2_RAT	PROTEIN BCL-2 ALPHA.	1.18e-22
10	206	13.3	192	1	BAXA_MOUSE	APOPTOSIS REGULATOR B	5.98e-18
11	194	12.5	192	1	BAXA_HUMAN	APOPTOSIS REGULATOR B	7.87e-16
12	189	12.2	218	1	BAXB_HUMAN	APOPTOSIS REGULATOR B	5.86e-15
13	176	11.3	350	6	MCLL_HUMAN	INDUCED MYELOID LEUKE	1.00e-12
14	165	10.6	142	1	BAXD_HUMAN	BAX PROTEIN, CYTOPLAS	7.08e-11
15	158	10.2	173	5	HEAL_MOUSE	HEMOPEPTIC, SPECIFIC	1.01e-09
16	126	8.1	179	3	EAR_ASFE4	APOPTOSIS REGULATOR B	1.00e-04
17	121	7.8	179	3	EAR_ASFE7	APOPTOSIS REGULATOR B	5.41e-04
18	118	7.6	179	3	EAR_ASFM2	APOPTOSIS REGULATOR B	1.46e-03
19	116	7.5	255	2	CON3_CAESL	CYTOCHROME C OXIDASE	2.80e-02
20	107	6.9	626	5	HTFG_BACSU	HEAT SHOCK PROTEIN HT	4.87e-02
21	106	6.8	133	4	GOP_BP44	GOP PPTEN.	6.63e-02
22	98	6.3	206	7	PEM2 YEAST	METHYLENE-FATTY-ACYL-	7.26e-01

P53563;
 01-OCT-1996 (REL. 34, CREATED)
 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCLX.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA MICHAELIDIS T.M.;
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -|- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.
 CC -|- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND
 CC BCL-X(S) ARE DERIVED BY ALTERNATIVE SPLICING.
 CC -|- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 DR EMBL; X82537; G607177; -.
 DR EMBL; X82537; G607178; -.
 KW APOPTOSIS; ALTERNATIVE SPLICING.
 FT VARSPLIC 126 188 MISSING (IN BCL-X(S)).
 SQ SEQUENCE 233 AA; 26130 MW; E0589815 CRC32;
 Query Match 16.3%; Score 254; DB 1; Length 233;
 Best Local Similarity 25.5%; Pred. No. 9.85e-27;
 Matches 36; Conservative 41; Mismatches 60; Indels 4; Gaps 4;
 Db 61 depavngatghs-saldarevipmaavkqalreagdefelyrrafsdltqhltpgta 119
 QY 48 EAEGVAAPADPEMTLPLOPSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLOPTAENA 107
 Db 120 yqsfqvvnelfrdgvnwrivaffsgalcvsvdkemqvlvsriaawmatylnhdh-1 178
 QY 108 YEYFKIATSLFESG-NWGRVVALFGYRLAHVYHGLTGLGQVTRFVVDMLHCCI 166
 Db 179 epwiqenggdwtdvlygna 199
 QY 167 ARWIAQRGGWVAALNL-GNGP 186
 RESULT 3
 ID BCLX_HUMAN STANDARD; PRT; 233 AA.
 AC Q07817;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE APOPTOSIS REGULATOR BCL-X.
 GN BCLX.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93364977.
 RA BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
 RA LINDSTEN T., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;
 RL CELL 74:597-608(1993).
 CC -|- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.
 CC BCL-X(S) ARE DERIVED BY ALTERNATIVE SPLICING.
 CC -|- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
 CC -|- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 DR EMBL; Z23116; G623237; -.
 DR EMBL; Z23115; G510901; -.
 DR MIN; 600039; -.
 DR PROSITE; PS01080; BCL2.
 KW APOPTOSIS; ALTERNATIVE SPLICING.
 FT VARSPLIC 126 188 MISSING (IN BCL-X(S)).
 FT CONFLICT 70 70 G -> A (IN G510901).

SQ SEQUENCE 233 AA; 26049 MW; 57C67491 CRC32;
 Query Match 16.1%; Score 250; DB 1; Length 233;
 Best Local Similarity 25.5%; Pred. No. 5.51e-26;
 Matches 36; Conservative 41; Mismatches 60; Indels 4; Gaps 4;
 Db 61 dspavngatghs-saldarevipmaavkqalreagdefelyrrafsdltqhltpgta 119
 QY 48 EAEGVAAPADPEMTLPLOPSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLOPTAENA 107
 Db 120 yqsfqvvnelfrdgvnwrivaffsgalcvsvdkemqvlvsriaawmatylnhdh-1 178
 QY 108 YEYFKIATSLFESG-NWGRVVALFGYRLAHVYHGLTGLGQVTRFVVDMLHCCI 166
 Db 179 epwiqenggdwtdvlygna 199
 QY 167 ARWIAQRGGWVAALNL-GNGP 186
 RESULT 4
 ID BCL2_CHICK STANDARD; PRT; 233 AA.
 AC Q00709;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE APOPTOSIS REGULATOR BCL-2.
 GN BCL-2
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92375724.
 RA EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
 RL NUCLEIC ACIDS RES. 20:4187-4192(1992).
 CC -|- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
 CC ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
 CC VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
 CC FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
 CC OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
 CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE
 CC (BY SIMILARITY).
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
 CC -|- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 DR EMBL; D11382; G222794; -.
 DR EMBL; D11381; G222794; JOINED.
 DR EMBL; Z11961; G52970; -.
 DR PIR; A37332; A37332.
 DR PIR; S24390; S24390.
 DR PROSITE; PS01080; BCL2.
 KW APOPTOSIS; TRANSMEMBRANE; MITOCHONDRION.
 FT TRANSMEM 208 228 POTENTIAL.
 FT CONFLICT 64 64 E -> S (IN REF. 2).
 FT CONFLICT 67 82 GSAAASEVPAEGLRP -> ARLLVRCPLRGCA
 FT CONFLICT 121 121 H -> T (IN REF. 2).
 FT CONFLICT 139 139 G -> V (IN REF. 2).
 SQ SEQUENCE 233 AA; 25687 MW; 3376502C CRC32;
 Query Match 15.8%; Score 245; DB 1; Length 233;
 Best Local Similarity 28.5%; Pred. No. 4.70e-25;
 Matches 41; Conservative 40; Mismatches 57; Indels 6; Gaps 6;
 Db 60 hhrpeppgsaaasevppae-glrrapp-g-vhlaalragdefsyrrafsdltqhltpgta 116
 QY 44 QOQEAEAGVAAPADPEMTLPLOPSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLOPT 103
 Db 117 pftahgrfvavveelfrdgvnwrivaffsgvvcvsvdkemqvlvsriaawmatylnhdh-1 176

QY	104	AENAYEYTKIATSLFESG-NWGRVVALLGFGYRLAHVYQHGLTGFLOGVTRFVVDFML	163
Db	177	rh-lhwiqdnnggdafvelgys	199
QY	163	HHCIARWIAQRGGWVAALNL-GNG	185
RESULT	5		
ID	BC2B_HUMAN	STANDARD;	PRT; 205 AA.
AC	P10416;		
DT	01-MAR-1989 (REL. 10, CREATED)		
DT	01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)		
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)		
DE	PROTEIN BCL-2-BETA.		
GN	BCL2.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA;		
OC	EUTHERIA; PRIMATES.		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE; 86259760.		
RA	TSUJIMOTO Y., CROCE C.M.;		
RL	PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).		
RN	[2]		
RN	REVISIONS TO 96 AND 110.		
RX	MEDLINE; 92375724.		
RA	EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;		
RL	NUCLEIC ACIDS RES. 20:4187-4192(1992).		
RN	[3]		
RN	SUBCELLULAR LOCATION.		
RX	MEDLINE; 91066924.		
RA	HOCKENBERY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;		
RL	NATURE 348:334-336(1990).		
CC	-1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE		
CC	ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF		
CC	VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT		
CC	FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES		
CC	OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.		
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.		
CC	-1- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE		
CC	II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION		
CC	T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE		
CC	REGIONS.		
CC	-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE		
CC	PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY		
CC	DIFFER AT THEIR C-TERMINAL ENDS.		
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.		
DR	EMBL; M13995; G179369; ALT_SEQ.		
DR	PIR; B29409; TVHUB1.		
DR	PIR; D37332; D37332.		
DR	MIM; 151430; -		
DR	PROSITE; PS01080; BCL2.		
KW	PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE;		
KW	MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.		
SEQ	SEQUENCE 205 AA; 22311 MW; ED321E5E CRC32;		
Query Match	15.48;	Score 239;	DB 1; Length 205;
Best Local Similarity	29.78;	Pred. No. 6.08e-24;	
Matches	38;	Conservative 34; Mismatches 51; Indels 5; Gaps	
Db	74	tpaagaaagpalsppvpvhlhlt--lrqagddfsryrddfaemssqhlhtpftargfa	131
QY	54	APADPENWTLP-LQPSMTGQVGRQLAIGDDINRRYDSEFTQMLQHLQPTAENAYEYTF	112
Db	132	tvveelfrdgvnvgriavaffefgvgmcvesvnmremspdvnlwmteylnrh-lhtwiq	190
QY	113	KIATSLFESG-NWGRVVALLGFGYRLAHVYQHGLTGFLOGVTRFVVDFMLHHCIAWTA	171
Db	191	dnngwgwa	198
QY	172	QRGGWAA	179


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QY 47 QAEAGVAAPADPEWTLPLQSSMTGQVGR-QLAIGDDINRRYDSEFQTMQLHQPTAE 105
D 122 targfatvveelfrdgwnvgrivaffegvmcvgvsnremspdvlnalwmtelylnrh 181
QY 106 NAYEFTKIATSLPESG-NWGRVALLGFGYRLAHVYQHGLTGLTGQVTRFVVDMLHH 164
D 182 -lhtwldqngdwafvel-ygsmrpl 206
QY 165 CIARWIAORGWGAALNLGNPI-LNV 191

RESULT 10
ID BAXA_MOUSE STANDARD; PRT; 192 AA.
AC Q07813;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN BAX.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X DBA/2 F1;
RX MEDLINE; 93364978.
RA OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
RL CELL 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L22473; G388162; -.
DR PIR; A47538; B47538.
DR MIN; 600040; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
FT TRANSMEM 172 192
FT POTENTIAL.
SQ SEQUENCE 192 AA; 21394 MW; BD035304 CRC32;

Query Match 13.3%; Score 206; DB 1; Length 192;
Best Local Similarity 25.6%; Pred. No. 5.98e-18;
Matches 46; Conservative 49; Mismatches 75; Indels 10; Gaps 8;

D 16 seqimktgafllqgfdragmagetpeltleqpqdstk-klseclrrigdelss-- 72
QY 31 TEEFVSXVYFRHQEQEAEAGVAAPADPEM-VTLPLQPSSTMGVGRQLAIGDDINRRY 89
D 73 nmelqrlmadvtdspre-vff-rvaadmfdgfnwgrvvalfyfasklklvkalctkvp 130
QY 90 DSEFQTMQLHQPTAEAYEFTKIATSLPESG-NWGRVALLGFGYRLAHVYQHGLT 147
D 131 elirtimgwtldf-lrerllvldqggwgllyfgtptwtgtvtfvavgltsaltlwk 189
QY 148 GFLGQVTRFVVDMLHHCIARWIAORGWGAALNLGNPI-LNV 191

RESULT 11
ID BAXA_HUMAN STANDARD; PRT; 192 AA.
AC Q07812;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN BAX.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-B-CELL;
RX MEDLINE; 93364978.
RA OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
RL CELL 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L22473; G388166; -.
DR PIR; A47538; A47538.
DR MIN; 600040; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
FT TRANSMEM 172 192
FT POTENTIAL.
SQ SEQUENCE 192 AA; 21184 MW; B2E6148A CRC32;

Query Match 12.5%; Score 194; DB 1; Length 192;
Best Local Similarity 24.5%; Pred. No. 7.87e-16;
Matches 40; Conservative 44; Mismatches 71; Indels 8; Gaps 6;

D 32 qdrgrmggeapelaldpvpqdstkklseclrrigdelss--nmelqrlmadvtds 89
QY 47 QAEAGVAAPADPEWTLPLQPSSTMGVGRQLAIGDDINRRYDSEFQTMQLHQPTAE 106
D 90 e-vff-rvaadmfdgfnwgrvvalfyfasklklvkalctkvpelirtimgwtldf-lre 146
QY 107 AYEFTKIATSLPESG-NWGRVALLGFGYRLAHVYQHGLTGLTGQVTRFVVDMLHH 164
D 147 rllgwdqggwgllyfgtptwtgtvtfvavgltsaltlwk 189
QY 165 CIARWIAORGWGAALNLGNPI-LNV 191

RESULT 12
ID BAXB_HUMAN STANDARD; PRT; 218 AA.
AC Q07814;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE APOPTOSIS REGULATOR BAX, CYTOPLASMIC ISOFORM BETA.
GN BAX.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-B-CELL;
RX MEDLINE; 93364978.
RA OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
RL CELL 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
CC APOPTOSIS REPRESSOR BCL-2.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L22474; G388168; -.
DR PIR; B47538; B47538.
DR MIN; 600040; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS; ALTERNATIVE SPLICING.
SQ SEQUENCE 218 AA; 24220 MW; 82B2FF09 CRC32;

Query Match 12.2%; Score 189; DB 1; Length 218;
Best Local Similarity 27.0%; Pred. No. 5.86e-15;
Matches 37; Conservative 35; Mismatches 58; Indels 7; Gaps 5;

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Db 32 qdragrmgepelaldvpqdstkklseclkrigdelids--nmelqrmiaavtdsdr 89
QY 47 QEAEGVAAPADPMTLPQPSTMGQVGRQLAIGDDINRRYDSEFQTMQLQHTAEN 106
Db 90 a-vff-rvaadmfsdgnfnwgrvvalvfasklvtlkalctkvpelirtimgwtldf- 146
QY 107 AYEYTKIATSLFESGN--WGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHH 164
Db 147 rllgwldqggwvrlk 163
QY 165 CIARWIAQRGGWVAALN 181

RESULT 13
ID MCL1_HUMAN STANDARD; PRT: 350 AA.
AC Q07820;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1.
GN MCL1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
SEQUENCE FROM N.A.
RC TISSUE-MYELOID LEUKEMIA CELLS;
RX MEDLINE; 93234528.
RA KOZOPAS K.M., YANG T., BUCHAN H.L., ZHOU P., CRAIG R.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:3516-3520(1993).
CC -|- FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTIATION AND
CC CONCOMITANT MAINTENANCE OF VIABILITY BUT NOT OF PROLIFERATION
CC (PROBABLE).
CC -|- INDUCTION: EXPRESSION INCREASES EARLY DURING PHORBOL-ESTER INDUCED
CC DIFFERENTIATION ALONG THE MONOCYTE/MACROPHAGE PATHWAY IN MYELOID
CC LEUKEMIA CELL LINES ML-1.
CC -|- SIMILARITY: BELONGS TO THE BCL2 FAMILY.
DR EMBL; L08246; -; NOT_ANNOTATED_CDS.
DR PIR; A47476; A47476.
DR MIM; 159552; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS; TRANSMEMBRANE; DIFFERENTIATION.
FT UNSURE 227 227 POTENTIAL.
FT TRANSMEM 330 349
SQ SEQUENCE 350 AA; 37365 MW; 10194B64 CRC32;

Query Match 11.3%; Score 176; DB 6; Length 350;
Best Local Similarity 24.3%; Pred. No. 1.00e-12;
Matches 34; Conservative 39; Mismatches 63; Indels 4; Gaps 3;

Db 174 lyrqlelslrlyreqatgaktkpmrgatsrkaletlrrvgdgvrnhetvfgmlr 233
QY 40 FYRHQOEAEAGVAAPADPMVTLPLQPSSTMGQVGRQ-LAIGDDINRRYDSEFQTMQLQ 98
Db 234 kldtknoddvkslsvmlhvfsgdvtngvrlvtlslsfafvakhkltinqesclepleas 293
QY 99 HLQPTAENAYEYTKIATSLFESG--NNGRVALLGFGYRLALHYVQHGLTGFLGQVTRF 156
Db 294 ltd-vlvrtktdwlvkqg 312
QY 157 VVDFMLHHCIARWIAQRGGW 176

RESULT 14
ID BAXD_HUMAN STANDARD; PRT: 143 AA.
AC P55269;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE BAX PROTEIN, CYTOPLASMIC ISOFORM DELTA.
GN BAX.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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OC EUTHERIA; PRIMATES.
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE; 95331797.
RA APTE S.S., MATTEI M.-G., OLSEN B.R.;
RL GENOMICS 26:592-594(1995).
CC -|- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -|- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; U19599; G841238; -.
DR MIM; 600040; -.
KW APOPTOSIS; ALTERNATIVE SPLICING.
SQ SEQUENCE 143 AA; 15772 MW; 71AA1CBD CRC32;

Query Match 10.6%; Score 165; DB 1; Length 143;
Best Local Similarity 27.4%; Pred. No. 7.08e-11;
Matches 29; Conservative 30; Mismatches 43; Indels 4; Gaps 3;

Db 36 tdsprevfrrvaadmfsdgnfnwgrvvalvfasklvtlkalctkvpelirtimgwtldf- 94
QY 104 AENAYEYTKIATSLFESGN--WGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFM 161
Db 95 lrerllgwldqggwgdgllsyfgtptwtvtfvavglvtasltiwlk 140
QY 162 LHHCIARWIAQRGGWVAALNGLNGFI-LNVLVGLVGLVGLGQVVR 206

RESULT 15
ID HSA1_MOUSE STANDARD; PRT: 172 AA.
AC Q07440;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN (A1 PROTEIN).
GN A1.
OS MUS SCULCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-CBA/J; TISSUE=BONE MARROW;
RX MEDLINE; 93346743.
RA LIN E.Y., ORLOFSKY A., BERGER M.S., PRYSTOWSKY M.B.;
RL J. IMMUNOL. 151:1979-1988(1993).
CC -|- FUNCTION: MAY FUNCTION IN THE RESPONSE OF HEMOPOIETIC CELLS TO
CC EXTERNAL SIGNALS.
CC -|- INDUCTION: BY GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR
CC AND LPS IN MACROPHAGES.
CC -|- SUBCELLULAR LOCATION: INTRACELLULAR.
CC -|- TISSUE SPECIFICITY: EXPRESSED IN HEMOPOIETIC TISSUES, INCLUDING
CC BONE MARROW, SPLEEN AND THYMUS.
CC -|- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
DR EMBL; L16462; G293274; -.
DR PROSITE; PS01080; BCL2.
KW APOPTOSIS.
FT DOMAIN 24 33 ALA/PRO-RICH.
SQ SEQUENCE 172 AA; 19914 MW; FFD38D6F CRC32;

Query Match 10.2%; Score 158; DB 5; Length 172;
Best Local Similarity 28.1%; Pred. No. 1.01e-09;
Matches 32; Conservative 29; Mismatches 46; Indels 7; Gaps 6;

Db 28 sapsqacrvlqrvaafsvqkeveklkaylddfhvestdarlfnqvmekfedglnwg 87
QY 69 STMGOVGRQLAIGDDINRRYDSEFQTMQLQHTAENAYEYTKIATSLFESG--NWG 125
Db 88 rivtifafigvllkklpqeqialdvcafkqsvsfvaefimnn-tgewirqggw 140
QY 126 RVALLGFG-YRLA-LHYVQHGLTG-FLGQVTRFVDFMLHHCIARWIAQRGGW 176

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• Thu Aug 21 17:44:06 1997

US-08-320-157-22.rsp

• Page 7

Search completed: Wed Aug 20 11:14:06 1997
Job time : 26 secs.

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